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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
 Run on: Fri Jan 21 14:30:17 2000; MasPar time 6.36 Seconds
 330.840 Million cell updates/sec
 Tabular output not generated.

Title: >US-09-176-546-2
 Description: (1-99) from US09176546.ppe
 Perfect Score: 682
 Sequence: 1 MADGSSDAAREPRAPAPR.....CQPLELAGLGFALQLDLCRQ 99
 Scoring table: PAM 150
 Gap 11

Searched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: a-geneseq35
 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
 14:part14 15:part15 16:part16 17:part17 18:part18
 19:part19 20:part20 21:part21 22:part22 23:part23
 24:part24 25:part25 26:part26 27:part27 28:part28
 29:part29 30:part30 31:part31 32:part32 33:part33
 34:part34 35:part35 36:part36 37:part37 38:part38
 39:part39

Statistics: Mean 28.682; Variance 122.478; scale 0.234

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB	ID	Description	Pred. No.
1	682	100.0	216	37	W2758		Modified human cardia	7.11e-55
2	682	100.0	216	29	W41573		Modified human cardia	7.11e-55
3	682	100.0	222	29	W41570		Modified human cardia	7.11e-55
4	680	99.7	226	26	W18054		Recombinant human myo	1.12e-54
5	678	99.4	319	29	W41572		Human cardiac troponi	1.75e-54
6	678	99.4	372	29	W41571		Cardiac troponin I/ca	1.75e-54
7	659	98.1	153	26	W18053		Recombinant myofibril	1.34e-53
8	536	78.6	80	21	W02286		Human troponin I frag	1.28e-40
9	239	35.0	38	12	R66181		Cardiac troponin I pe	2.16e-12
10	233	34.2	35	21	W02285		Human troponin I frag	7.62e-12
11	207	30.4	31	32	W37924		N-terminal amino acid	1.73e-09
12	202	29.6	30	11	R55781		Human cardiac troponi	4.88e-09
13	202	29.6	31	21	W05041		N-terminus of cardiac	4.88e-09
14	202	29.6	31	14	R73052		N-terminal sequence o	4.88e-09
15	201	29.5	182	26	W22598		Human fast twitch ske	5.99e-09
16	173	25.4	26	11	R55786		Human cardiac troponi	1.83e-06

17	139	20.4	24	11	R66736	Synthetic immunogen b	1.56e-03
18	129	18.9	18	12	R66183	Cardiac troponin I pe	1.08e-02
19	127	18.6	39	32	W65159	Synthetic bi-epitopic	1.58e-02
20	126	18.5	38	32	W65160	Synthetic bi-epitopic	1.91e-02
21	112	16.4	35	32	W65158	Synthetic bi-epitopic	2.66e-01
22	110	16.1	33	32	W65157	Synthetic bi-epitopic	3.84e-01
23	104	15.2	24	32	W65161	Synthetic bi-epitopic	1.15e+00
24	103	15.1	20	25	W30854	Human cardiac troponi	1.38e+00
25	101	14.8	258	26	W22599	Human fast twitch ske	1.99e+00
26	100	14.7	28	32	W65156	Synthetic bi-epitopic	2.38e+00
27	100	14.7	29	32	W65162	Synthetic bi-epitopic	2.38e+00
28	94	13.8	374	2	P80277	Sequence encoded by 3	6.93e+00
29	93	13.6	27	32	W65155	Synthetic bi-epitopic	8.27e+00
30	92	13.5	111	1	P81515	Bovine Bone Morphogen	9.86e+00
31	87	12.8	716	1	P81099	Sequence of Rhodospir	2.35e+01
32	87	12.8	716	1	P83141	Sequence of L-phenyla	2.35e+01
33	87	12.8	716	13	R70682	Stabilised phenylalan	2.35e+01
34	87	12.8	716	1	P80513	L-phenylalanine ammon	2.35e+01
35	87	12.8	716	1	P95783	L-phenylalanine ammon	2.79e+01
36	86	12.6	13	12	R66182	Cardiac troponin I pe	3.31e+01
37	85	12.5	657	6	R29580	EMR-1 gene product..	3.93e+01
38	84	12.3	183	39	W89689	Murine osteogenic pro	3.93e+01
39	84	12.3	183	12	R51643	Mature mouse CBMP3.	3.93e+01
40	84	12.3	183	8	R44756	Murine osteogenic pro	3.93e+01
41	84	12.3	183	16	R85764	Mature murine CBMP3.	3.93e+01
42	84	12.3	183	29	W43112	Murine osteogenic pro	3.93e+01
43	84	12.3	432	13	R77865	S. clavuligerus ORF8	3.93e+01
44	84	12.3	436	21	W03662	Human 70K UI snRNP pr	3.93e+01
45	84	12.3	614	15	R82630	70K autoantigen, part	3.93e+01

ALIGNMENTS

RESULT 1

ID W2758 standard; Protein: 216 AA.

AC W2758;

DT 13-JAN-1999 (first entry)

DE Modified human cardiac troponin I.

KW Human cardiac troponin I; troponin I.

KW stable troponin subunit; cardiac disorder; myocardial damage;

KW heart attack.

OS Homo sapiens.

PS Synthetic.

PN US5834210-A.

PD 10-NOV-1998.

PF 31-OCT-1997; 961858.

PR 31-OCT-1997; US-961858.

PR 23-MAY-1997; US-862613.

PPA (SPEPC-) SPECTRAL DIAGNOSTICS INC.

PI Liu S, Shi Q.

DR WPI: 99-008702/01.

DR N-PSDB; V67262.

PT Recombinant modified human cardiac troponin I and complexes with

troponin T and C - for use in assays to determine levels of these

proteins, as control values in determining extent of cardiac damage

PT e.g. in heart attacks

PS Claim 2; Fig 1; 16pp; English.

CC The present sequence represents modified human cardiac troponin I.
 CC Expression in Escherichia coli of the modified troponin I is increased
 CC compared to that of the native sequence. The modified troponin I
 CC consists of the native troponin I protein sequence with an N-terminal
 CC extension of 5-8 residues, including an N-terminal methionine. The
 CC present invention describes troponin protein complexes which are useful
 CC for the determination of myocardial damage. Troponin I and troponin T
 CC have been found to be highly specific markers for cardiac disorders,
 CC especially heart attacks. They must be complexed with troponin C to form
 CC a stable structure, which is difficult to isolate. Recombinant
 CC preparation of the trimeric structure allows sufficient quantities to be
 CC obtained, so that assays can be performed to accurately determine
 CC quantification of troponin complex levels for e.g. control values. The
 CC complex can also be used as an antigen to raise antibodies.
 SQ Sequence 216 AA;

Query Match 100.0%; Score 682; DB 37; Length 216;
 Best Local Similarity 100.0%; Pred. No. 7.11e-55;
 Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 7 madgssdaareppapapirrrssnyrayatephakkskissarqlgltlllqiaqke 66
 QY 1 MADGSSDAAREPPAPAPIRRRSSNYRAYATEPHAKKSKISASRKLQKLTLLQIAQKE 60

Db 67 lereaeerrgekgalstrcqpelaglgfaelqdlcrq 105
 QY 61 LEREAEERRGEGKALSTRCPQLELAGLFAELQDLCRQ 99

RESULT 2

ID W41573 standard; Protein: 216 AA.

AC W41573;

DT 22-JUN-1998 (first entry)

DE Modified human cardiac troponin I HcTnI-(HL)3.

KW Troponin I; immunoassay; assay; analysis; human; cardiac muscle;

KW skeletal muscle; injury; myocardial infarction; diagnosis;

KW HcTnI-(HL)3.

OS Homo sapiens.

OS Synthetic.

PH Key Location/Qualifiers

FT Protein 1..210

FT Peptide /label= HcTnI

FT 211..216

FT /label= (HL)3

FT /note= "(Claim 23)"

PN W09739132-A1.

PD 23-OCT-1997.

PF 14-APR-1997; U06147.

PR 11-APR-1997; US-833743.

PR 16-APR-1996; US-015772.

PA (UYMI-) UNIV MIAMI.

PI Potter JD;

DR WPI: 98-062676/06.

DR N-PSDB: V04230.

PT Immunoassay of mammalian troponin using stable standard for comparison - specifically acid-dialysed solution or its lyophilisate used for diagnosis of cardiac or skeletal muscle damage

PS Example 5; Page 74-75; 94pp; English.

CC This polypeptide comprises a C-terminally modified cardiac troponin I protein, designated HcTnI-(HL)3, comprising human cardiac troponin I (HcTnI) modified to add an alternating 3 histidine 3 leucine tag (see W41569). This modification alters the isoelectric point of

CC the protein, thereby improving its solubility and stability. A polynucleotide (see V04230) encoding the modified HcTnI was produced by PCR amplification of a HcTnI cDNA template, and was inserted into

CC vector pET lld to allow expression of HcTnI-(HL)3 in Escherichia coli transformants. The invention provides an assay for measuring mammalian, preferably human, troponin in a patient sample. The

CC assay involves comparing the level in the sample with a novel troponin protein standard. This is a storage stable, soluble troponin, a functional fragment of the troponin, a modified troponin

CC or its functional fragment, a troponin fusion protein or a hetero-multimeric troponin complex (see W41570-75). The method is used to monitor changes in the level of human troponin, particularly for

CC diagnosis of diseases involving damage to heart or skeletal muscle, e.g. acute myocardial infarction. It may also be used to study normal and pathological functions of troponin-expressing tissues.

SQ Sequence 216 AA;

Query Match 100.0%; Score 682; DB 29; Length 216;

Best Local Similarity 100.0%; Pred. No. 7.11e-55;

Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 madgssdaareppapapirrrssnyrayatephakkskissarqlgltlllqiaqke 60
 QY 1 MADGSSDAAREPPAPAPIRRRSSNYRAYATEPHAKKSKISASRKLQKLTLLQIAQKE 60

Db 61 lereaeerrgekgalstrcqpelaglgfaelqdlcrq 99

QY 61 LEREAEERRGEGKALSTRCPQLELAGLFAELQDLCRQ 99

RESULT 3

ID W41570 standard; Protein: 222 AA.

AC W41570;

DT 22-JUN-1998 (first entry)

DE Modified human cardiac troponin I HcTnI-K6-H5-D.

KW Troponin I; immunoassay; assay; analysis; human; cardiac muscle;

KW skeletal muscle; injury; myocardial infarction; diagnosis;

KW HcTnI-K6-H5-D.

OS Homo sapiens.

OS Synthetic.

PN W09739132-A1.

PD 23-OCT-1997.

PF 14-APR-1997; U06147.

PR 11-APR-1997; US-833743.

PR 16-APR-1996; US-015772.

PA (UYMI-) UNIV MIAMI.

PI Potter JD;

DR WPI: 98-062676/06.

DR N-PSDB: V04221.

PT Immunoassay of mammalian troponin using stable standard for

PT comparison - specifically acid-dialysed solution or its lyophilisate

PT used for diagnosis of cardiac or skeletal muscle damage

PS Example 2; Page 64-65; 94pp; English.

CC This polypeptide comprises a C-terminally modified cardiac troponin I protein, designated HcTnI-K6-H5-D, comprising human cardiac troponin I (HcTnI) modified to add 6 lysines, 5 histidines and one aspartate residue. This modification was made to alter the isoelectric point

CC of the protein, thereby improving its solubility and stability. A polynucleotide (see V04221) encoding the modified HcTnI was produced by PCR amplification of a HcTnI cDNA template, and was inserted into

CC vector pET lld to allow expression of HcTnI-K6-H5-D in Escherichia coli transformants. The invention provides an assay for measuring mammalian, preferably human, troponin in a patient sample. The

CC assay involves comparing the level in the sample with a novel troponin protein standard. This is a storage stable, soluble troponin, a functional fragment of the troponin, a modified troponin

CC or its functional fragment, a troponin fusion protein or a hetero-multimeric troponin complex (see W41570-75). The method is used to monitor changes in the level of human troponin, particularly for

CC diagnosis of diseases involving damage to heart or skeletal muscle, e.g. acute myocardial infarction. It may also be used to study normal and pathological functions of troponin-expressing tissues.

SQ Sequence 222 AA;

Query Match 100.0%; Score 682; DB 29; Length 222;

Best Local Similarity 100.0%; Pred. No. 7.11e-55;

Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 madgssdaareppapapirrrssnyrayatephakkskissarqlgltlllqiaqke 60
 QY 1 MADGSSDAAREPPAPAPIRRRSSNYRAYATEPHAKKSKISASRKLQKLTLLQIAQKE 60

Db 61 lereaeerrgekgalstrcqpelaglgfaelqdlcrq 99

QY 61 LEREAEERRGEGKALSTRCPQLELAGLFAELQDLCRQ 99

RESULT 4

ID W18054 standard; protein: 226 AA.

AC W18054;

DT 20-FEB-1998 (first entry)

DE Recombinant human myofibrillar contractile protein Troponin I.

KW Cardiac isotype; myofibrillar contractile protein; Troponin I; cTnI; inhibitory subunit; thin filament regulatory protein; TnI immunoassay; calcium sensitivity; cardiac muscle; striated muscle; degradation product; cyanogen bromide cleavage; myocardial infarction; immunological activity.

OS Synthetic.

OS Homo sapiens.

PH Key Location/Qualifiers

FT Modified_site 87 /note= "carboxymethylated to prevent dimerisation by
FT FT inter or intra disulphide bridges"
FT Modified_site 104 /note= "carboxymethylated to prevent dimerisation by
FT FT inter or intra disulphide bridges"
FT Peptide 9..217 /note= "human Troponin I"
FT FT
FT Peptide 9..161 /note= "CN-Br cleavage fragment"
FT FT
FT Peptide 8..219 /note= "CN-Br cleavage fragment"
FT FT
FT Peptide 2..4 /note= "CN-Br cleavage fragment"
FT FT
FT Peptide 5..8 /note= "CN-Br cleavage fragment"
FT FT
FT Peptide 163..208 /note= "CN-Br cleavage fragment"
FT FT
FT Peptide 209..119 /note= "CN-Br cleavage fragment"
FT FT
FT Peptide 220..226 /note= "CN-Bf cleavage fragment"
FT FT
FT Peptide 14..101 /note= "CN-Br cleavage fragment"
FT FT
PN WO9719955-A1.
PD 05-JUN-1997.
PF 26-NOV-1996; U18878.
PR 29-NOV-1995; US-564526.
PA (DADE-) DADE INT INC.
PI Demarco C, Morjana NA;
DR WPI: 97-310526/28.
PT Human cardiac Troponin I cyanogen bromide cleaved fragment - used in
PT calibrator or control for troponin I immunoassay
PS Disclosure: Page 20; 52pp; English.
CC The present sequence represents a recombinant form of the cardiac
CC isotype of the myofibrillar contractile protein Troponin I (cTnI).
CC Troponin I is the inhibitory subunit of Troponin, a thin filament
CC regulatory protein complex which confers calcium sensitivity to the
CC cardiac and striated muscle. cTnI was cleaved with cyanogen bromide,
CC which cleaves at Met residues with a high specificity under acidic
CC conditions, to generate several fragments. A 153 amino acid CNBr-cTnI
CC isoform is used in a calibrator or a control for a TnI immunoassay. The
CC CNBr-cTnI isoform is comparable in molecular weight to a major
CC degradation product of native cTnI in the serum of patients who have
CC experienced myocardial infarction. The peptide has immunological activity
CC to antibodies against TnI. The CNBr-cTnI isoform has an average of 3-4
CC times more reactivity than TnI and lower non-specific binding, as
CC measured by radial partition immunoassay. It also has increased stability
CC over the synthetic peptide currently used in the Dade TnI immunoassay.
SQ Sequence 226 AA;

Query Match 99.7%; Score 680; DB 26; Length 226;
Best Local Similarity 99.0%; Pred. No. 1.12e-54;
Matches 98; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 8 madgssdaareppapaparrssnyravatephakkskisarklqltlllqakqe 67
QY 1 MADGSSDAAREPPAPAPARRSSNYRATATEPHAKKSKISARKLQLTLLQIAKQE 60
Db 68 lereaeerrgekgalstrcqpeltglgfaelqdlcrq 106
QY 61 LEREAEERGERGKALSTRCPLELAGLGFALQDLQCRQ 99

RESULT 5
ID W41572 standard; Protein; 319 AA.
AC W41572;
DT 22-JUN-1998 (first entry)
DE Human cardiac troponin I/carp parvalbumin fusion protein.
KW Troponin I; parvalbumin; immunoassay; assay; analysis; human;
KW cardiac muscle; skeletal muscle; injury; myocardial infarction;
KW diagnosis; HcTnI; carp.
OS Chimeric - Homo sapiens.

OS Chimeric - Cyprinus carpio.
FH Key Location/Qualifiers
FT Protein 1..210
FT /label= HcTnI
FT 211..319
FT /label= Parvalbumin
PN WO9739132-A1.
PD 23-OCT-1997.
PF 14-APR-1997; U06147.
PR 11-APR-1997; US-833743.
PR 16-APR-1996; US-015772.
PA (UYMI-) UNIV MIAMI.
PI Potter JD;
DR WPI: 98-062676/06.
DR N-PSDB: V04228.
PT Immunoassay of mammalian troponin using stable standard for
PT comparison - specifically acid-dialysed solution or its lyophilisate
PT used for diagnosis of cardiac or skeletal muscle damage
PS Example 4; Page 71-72; 94pp; English.
CC This polypeptide comprises fusion protein with the N-terminal
CC region being human cardiac troponin I (HcTnI) and the C-terminal
CC region being carp parvalbumin. It was expressed in E. coli host
CC cells utilising a vector incorporating a polynucleotide (see
CC V04228) encoding the fusion. The addition of parvalbumin, a
CC calcium binding protein, to HcTnI provides more favourable solubility
CC properties to HcTnI and to the fusion protein. The invention
CC provides an assay for measuring mammalian, preferably human,
CC troponin in a patient sample. The assay includes the step of
CC comparing the level in the sample with a novel troponin protein
CC standard. This may be a storage stable, soluble mammalian troponin,
CC a functional fragment of the troponin, a modified troponin or its
CC functional fragment, a troponin fusion protein or a heteromultimeric
CC troponin complex (see also W41570-75). The method is used to
CC monitor changes in the level of human troponin, particularly for
CC diagnosis of diseases involving damage to heart or skeletal muscle,
CC e.g. acute myocardial infarction. It may also be used to study
CC normal and pathological functions of troponin-expressing tissues.
SQ Sequence 319 AA;

Query Match 99.4%; Score 678; DB 29; Length 319;
Best Local Similarity 99.0%; Pred. No. 1.75e-54;
Matches 98; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 mvdgssdaareppapaparrssnyravatephakkskisarklqltlllqakqe 60
QY 1 MADGSSDAAREPPAPAPARRSSNYRATATEPHAKKSKISARKLQLTLLQIAKQE 60
Db 61 lereaeerrgekgalstrcqpeltglgfaelqdlcrq 99
QY 61 LEREAEERGERGKALSTRCPLELAGLGFALQDLQCRQ 99

RESULT 6
ID W41571 standard; Protein; 372 AA.
AC W41571;
DT 22-JUN-1998 (first entry)
DE Cardiac troponin I/cardiac troponin C fusion protein.
KW Troponin I; troponin C; immunoassay; assay; analysis; human;
KW cardiac muscle; skeletal muscle; injury; myocardial infarction;
KW diagnosis; HcTnI; HcTnC.
OS Homo sapiens.

FH Key Location/Qualifiers
FT Protein 1..210
FT /label= HcTnI
FT 211..372
FT /label= HcTnC
PN WO9739132-A1.
PD 23-OCT-1997.
PF 14-APR-1997; U06147.
PR 11-APR-1997; US-833743.
PR 16-APR-1996; US-015772.
PA (UYMI-) UNIV MIAMI.
PI Potter JD;

DR WPI; 98-062676/06.
 DR N-ESDB; V04225.
 PT Immunooassay of mammalian troponin using stable standard for
 PT comparison - specifically acid-dialysed solution or its lyophilisate
 PT used for diagnosis of cardiac or skeletal muscle damage
 PS Example 3; Page 67-68; 94pp; English.
 CC This protein sequence comprises a fusion protein with the
 CC the N-terminal region being human cardiac troponin I (HcTnI) and
 CC the C-terminal region being human cardiac troponin C (HcTnC). It
 CC has been expressed in E. coli host cells utilising a vector
 CC carrying a HcTnI-HcTnC polynucleotide (see V04225) obtained by PCR.
 CC The addition of the calcium binding protein HcTnC to HcTnI provided
 CC more favourable solubility properties to HcTnI. The invention
 CC provides an assay for measuring mammalian, preferably human,
 CC troponin in a patient sample. The assay includes the step of
 CC comparing the level in the sample with a novel troponin protein
 CC standard. This may be a storage stable, soluble mammalian troponin,
 CC a functional fragment of the troponin, a modified troponin or its
 CC functional fragment, a troponin fusion protein or a heteromultimeric
 CC troponin complex (see also W41570-75). The method is used to
 CC monitor changes in the level of human troponin, particularly for
 CC diagnosis of diseases involving damage to heart or skeletal muscle,
 CC e.g. acute myocardial infarction. It may also be used to study
 CC normal and pathological functions of troponin-expressing tissues.
 CC Sequence 372 AA;
 SQ

Query Match 99.4%; Score 678; DB 29; Length 372;
 Best Local Similarity 99.0%; Pred. No. 1.75e-54;
 Matches 98; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 mvdgsdaareprpapapirrrssnyrayatephakkkksasrkqlklllqiaqke 60
 QY 1 MADGSSDAAREPRPAPAPIRRRSSNYRAYATEPHAKKKKSASRKQLKLLQLIAQKE 60

Db 61 lereaeergekgralstrcqpelaglgfaelqdlcrq 99
 QY 61 LEREAEERGEKGRALSTRCQPLEAGLGFAELQDLCRQ 99

RESULT 7
 ID W18053 standard; protein; 153 AA.
 AC W18053;
 DT 20-FEB-1998 (first entry)
 DE Recombinant myofibrillar contractile protein Troponin I CN-Br fragment.
 KW Cardiac isotype; myofibrillar contractile protein; Troponin I; ctni;
 KW inhibitory subunit; thin filament regulatory protein; Tni immunoassay;
 KW calcium sensitivity; cardiac muscle; striated muscle;
 KW degradation product; cyanogen bromide cleavage; myocardial infarction;
 KW immunological activity.
 OS Synthetic.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Modified_site 79
 FT /note= "carboxymethylated to prevent dimerisation by
 FT inter or intra disulphide bridges"
 FT Modified_site 96
 FT /note= "carboxymethylated to prevent dimerisation by
 FT inter or intra disulphide bridges"
 FT W09719955-Al.
 PN 05-JUN-1997.
 PF 26-NOV-1996; U18878.
 PR 29-NOV-1995; US-564526.
 PA (DADE-) DADE INT INC.
 PI Demarco C, Morjana NA;
 DR WPI; 97-310526/28.
 PT Human cardiac Troponin I cyanogen bromide cleaved fragment - used in
 PT calibrator or control for troponin I immunoassay
 PS Disclosure: Page 20; 52pp; English.
 CC The present sequence represents a CN-Br cleavage fragment of the
 CC recombinant cardiac isotype of the myofibrillar contractile protein
 CC troponin I (ctni). Troponin I is the inhibitory subunit of troponin,
 CC a thin filament regulatory protein complex which confers calcium
 CC sensitivity to the cardiac and striated muscle. The present 153 amino

CC acid CNBr-ctni isoform is used in a calibrator or a control for a Tni
 CC immunoassay. The CNBr-ctni isoform is comparable in molecular weight to
 CC a major degradation product of native ctni in the serum of patients who
 CC have experienced myocardial infarction. The peptide has immunological
 CC activity to antibodies against Tni. The CNBr-ctni isoform has an average
 CC of 3-4 times more reactivity than rTni and lower non-specific binding, as
 CC measured by radial partition immunoassay. It also has increased stability
 CC over the synthetic peptide currently used in the Bade Tni immunoassay.
 CC Sequence 153 AA;
 SQ

Query Match 98.1%; Score 669; DB 26; Length 153;
 Best Local Similarity 99.0%; Pred. No. 1.34e-53;
 Matches 97; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 adgssdaareprpapapirrrssnyrayatephakkkksasrkqlklllqiaqkel 60
 QY 2 ADGSSDAAREPRPAPAPIRRRSSNYRAYATEPHAKKKKSASRKQLKLLQLIAQKEL 61

Db 61 ereaeergekgralstrcqpelaglgfaelqdlcrq 98
 QY 62 EREAERGEKGRALSTRCQPLEAGLGFAELQDLCRQ 99

RESULT 8
 ID W02286 standard; peptide; 80 AA.
 AC W02286;
 DT 27-MAY-1997 (first entry)
 DE Human troponin I fragment, residues 2-81 (initial Met is residue 1).
 KW Cardiac; heart; troponin I; fragment; analyte; aqueous calibrator;
 KW stabiliser; myosin; myoglobin; lactate dehydrogenase; creatine kinase;
 KW myocardial infarction; heart attack.
 OS Homo sapiens.
 PN W09627661-Al.
 PD 12-SEP-1996.
 PF 06-MAR-1996; U03034.
 PR 07-MAR-1995; US-400158.
 PA (DADE-) DADE INT INC.
 PI Bauer R, Chin B, Flaa C, Sabucedo A;
 DR WPI; 96-425423/42.
 PT Aq. compsn. for stabilising proteins for use as controls for cardiac
 PT markers - comprising buffer, reducing agent, stabilising protein,
 PT chelating agent and salt
 PS Claim 6; Page 41; 57pp; English.
 CC W02285 and W02286 are troponin I fragments used to exemplify the
 CC usefulness of an aqueous composition (may be lyophilised) used as an
 CC aqueous calibrator and control solution for diagnostic assays for
 CC cardiac proteins and peptides. The stabilising solution comprises a
 CC buffer, a reducing agent (e.g. 2-mercaptoethanol or N-acetyl-cysteine),
 CC a stabilising protein (e.g. albumin or casein), a chelating agent (e.g.
 CC EDTA or EGTA) a salt (e.g. NaCl), a blocking agent (especially gelatin)
 CC and a bulking agent (e.g. trehalose, glucose, sucrose, galactose, etc.)
 CC The composition is especially useful for diagnostic assays of
 CC troponin, myoglobin, creatine kinase (CK), CK isoenzymes, lactate
 CC dehydrogenase (LD), LD isoenzymes, myosin and fragments of these. The
 CC composition may be used, e.g. in tests for acute myocardial infarction.
 CC The stabilising composition is not derived from human serum, and thus
 CC prevents exposure of the user (and manufacturing personnel) to many of
 CC the diseases which can be spread by contact with human blood products.
 CC The composition is also able to keep analytes stable in liquid form for
 CC extended periods of time.
 CC Sequence 80 AA;
 SQ

Query Match 78.6%; Score 536; DB 21; Length 80;
 Best Local Similarity 100.0%; Pred. No. 1.28e-40;
 Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 adgssdaareprpapapirrrssnyrayatephakkkksasrkqlklllqiaqkel 60
 QY 2 ADGSSDAAREPRPAPAPIRRRSSNYRAYATEPHAKKKKSASRKQLKLLQLIAQKEL 61

Db 61 ereaeergekgralstrcqpelaglgfaelqdlcrq 80
 QY 62 EREAERGEKGRALSTRCQPLEAGLGFAELQDLCRQ 81

CC the diseases which can be spread by contact with human blood products.
 CC The composition is also able to keep analytes stable in liquid form for
 CC extended periods of time.

RESULT 9

ID R66181 standard; peptide: 38 AA.
 AC R66181;
 DT 21-JUL-1995 (first entry)
 DE Cardiac troponin I peptide fragment #1.
 KW Cardiac troponin I; skeletal troponin I; immunoassay; antibody;
 KW myocardial damage; myocardial infarction.
 OS Synthetic.
 PN WO9427156-A.
 PD 24-NOV-1994.
 PF 16-MAY-1994; U05468.
 PR 17-MAY-1993; US-063168.
 PA (FORT-) FORTON BIOSCIENCE INC.
 PI Torretti SA, Vargas AM, Wicks RW, Zartman LO;
 DR WPI: 95-006973/01.
 PT Quantitative assay of cardiac troponin I - for diagnosis of
 PT myocardial damage, esp. infarction, also new antibodies specific
 PT for cardiac but not skeletal troponin I
 PS Claim 12; Page 21; 31pp; English.
 CC The sequences given in R66181-83 represent peptides which are
 CC derived from cardiac troponin I but which are not present in skeletal
 CC troponin I. These peptides may be used in an immunoassay for the
 CC quantitation of cardiac troponin I in a biological fluid. These
 CC peptides bind antibodies specific for cardiac troponin I and may be
 CC used to confirm diagnosis of myocardial damage, esp. myocardial
 CC infarction.
 SQ Sequence 38 AA;

Query Match 35.0%; Score 239; DB 12; Length 38;
 Best Local Similarity 97.4%; Pred. No. 2.16e-12;
 Matches 38; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Db 1 madgssdaareppapapirrr-ssnyrayatephakhs 38
 |||||
 QY 1 MADGSSDAAREPPAPAPIRRRSSNYRAYATEPHAKHS 39

RESULT 10

ID W02285 standard; peptide: 35 AA.
 AC W02285;
 DT 27-MAY-1997 (first entry)
 DE Human troponin I fragment, residues 27-61 (initial Met is residue 1).
 KW Cardiac; heart; troponin I; fragment; analyte; aqueous calibrator;
 KW stabiliser; myosin; myoglobin; lactate dehydrogenase; creatine kinase;
 KW myocardial infarction; heart attack.
 OS Homo sapiens.
 PN WO9627661-A1.
 PD 12-SEP-1996.
 PF 06-MAR-1996; U03034.
 PR 07-MAR-1995; US-400158.
 PA (DADE-) DADE INT INC.
 PI Bauer, R, Chin B, Flaa C, Sabucedo A;
 DR WPI: 96-425423/42.
 PT Aq. compsn. for stabilising proteins for use as controls for cardiac
 PT markers - comprising buffer, reducing agent, stabilising protein,
 PT chelating agent and salt
 PS Claim 5; Page 40; 57pp; English.
 CC W02285 and W02286 are troponin I fragments used to exemplify the
 CC usefulness of an aqueous composition (may be lyophilised) used as an
 CC aqueous calibrator and control solution for diagnostic assays for
 CC cardiac proteins and peptides. The stabilising solution comprises a
 CC buffer, a reducing agent (e.g. 2-mercaptoethanol or N-acetyl-cysteine),
 CC a stabilising protein (e.g. albumin or casein), a chelating agent (e.g.
 CC EDTA or EGTA) a salt (e.g. NaCl), a blocking agent (especially gelatin)
 CC and a bulking agent (e.g. trehalose, glucose, sucrose, galactose, etc.)
 CC The composition is especially useful for diagnostic assays of
 CC troponin, myoglobin, creatine kinase (CK), CK isoenzymes, lactate
 CC dehydrogenase (LD), LD isoenzymes, myosin and fragments of these. The
 CC composition may be used, e.g. in tests for acute myocardial infarction.
 CC The stabilising composition is not derived from human serum, and thus
 CC prevents exposure of the user (and manufacturing personnel) to many of

Query Match 34.2%; Score 233; DB 21; Length 35;
 Best Local Similarity 100.0%; Pred. No. 7.62e-12;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 rayatephakhsksasrklqlklllqakael 35
 |||||
 QY 27 RAYATEPHAKHSKSISASRKLQLKLLQLIAKQEL 61

RESULT 11

ID W37924 standard; peptide: 31 AA.
 AC W37924;
 DT 09-SEP-1998 (first entry)
 DE N-terminal amino acid sequence of cardiac troponin I.
 KW Cardiac troponin I; cTnI; acute myocardial infarction; inhibition;
 KW Cardiac troponin I; cTnI; cardio-specific marker.
 OS Homo sapiens.
 PN WO9816255-A2.
 PD 23-APR-1998.
 PF 15-OCT-1997; U18368.
 PR 15-OCT-1997; US-730111.
 PR 15-OCT-1996; US-730111.
 PA (NAVI-) NAVIX INC.
 PI Botyanszki J, Dave KI, Sintar E;
 DR WPI: 98-251059/22.
 PT Stabilising individual sub-units of multimeric protein by attaching
 PT to polymer - particularly cardiac troponin sub-units for use as
 PT controls in immunoassays for diagnosis of acute myocardial infarction
 PS Disclosure; Page 14; 34pp; English.
 CC This is the amino acid sequence of the N-terminal sequence of the
 CC cardiac troponin I (cTnI) protein, acts as an inhibitory subunit to
 CC cardiac troponin T (cTnT), which is released after an acute
 CC myocardial infarction. The cTnI and cTnT are useful as
 CC cardio-specific markers, particularly for early diagnosis of acute
 CC myocardial infarction by immunoassays. The stabilised subunits are
 CC used as control reagents in such assays.
 SQ Sequence 31 AA;

Query Match 30.4%; Score 207; DB 32; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.73e-09;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 madgssdaareppapapirrrssnyrayat 31
 |||||
 QY 1 MADGSSDAAREPPAPAPIRRRSSNYRAYAT 31

RESULT 12

ID R55781 standard; peptide: 30 AA.
 AC R55781;
 DT 21-FEB-1995 (first entry)
 DE Human cardiac troponin I N-terminal sequence.
 KW Human cardiac troponin I; heart muscle necrosis; immunogen; epitope;
 KW immunodiagnosis; acute myocardial infarction.
 OS Homo sapiens.
 PN DE4243648-A.
 PD 07-JUL-1994.
 PF 23-DEC-1992; 243648.
 PR 23-DEC-1992; DE-243648.
 PA (BOEF) BOEHRINGER MANNHEIM GMBH.
 PI Borjya A, Donie F, Lill H, Seidel C;
 DR WPI: 94-218764/27.
 PT Rapid diagnosis of heart muscle necrosis in myocardial infarction
 PT - by immunological test using new antibody recognising cardiac
 PT troponin I N-terminal peptide
 PS Claim 1; Page 8; 12pp; German.
 CC The N-terminal 30 amino acids of human cardiac troponin I (R55781)
 CC or subfragments of it (R55782-R55788) can be used as immunogens. The

CC antibodies raised by immunising animals (pref. sheep) with the
CC peptides are useful for rapid diagnosis of heart muscle necrosis.
SQ Sequence 30 AA;

Query Match 29.6%; Score 202; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.88e-09;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 madgssdaareppapapirrrssnyraya 30
|||||
Qy 1 MADGSSDAAREPPAPAPIRRRSSNYRAYA 30

RESULT 13

ID W05041 standard; peptide; 31 AA.
AC W05041;
DT 12-JUN-1997 (first entry)
DE N-terminus of cardiac troponin I.
KW Cardiac troponin I; N-terminus; protease; inhibitor; cathepsin protease;
KW cardiac tissue; serine protease; cysteine protease; aspartate protease;
KW aminopeptidase protease; metalloendo-peptidase; myocardial infarction;
KW human.
OS Homo sapiens.
PN US9560937-A.
PD 01-OCT-1996.
PF 24-AUG-1993; 110824.
PR 24-AUG-1993; US-110824.
PR 26-AUG-1994; US-296644.
PA (SPEC-) SPECTRAL DIAGNOSTICS INC.
PI Jackowski G, Lee L;
DR WPI: 96-454492/45.
PT Purifying human cardiac troponin I - by extn. of human cardiac
PT tissue with a buffer contg. a protease inhibitor mixt. and affinity
PT chromatography
PS Claim 8; Column 13-14; 12pp; English.
CC This sequence represents the N-terminus of human cardiac troponin I. The
CC degradation of this sequence is inhibited by the protease inhibitor
CC mixture used in the method of the invention. The method of the invention
CC is for isolating a pure, stable cardiac troponin I preparation, where the
CC troponin I has a molecular weight of about 28 kDa. The method comprises
CC extracting human cardiac tissue with an aqueous extraction buffer at a pH
CC of 7 to 9 which is 8 to 10 M in urea and contains a protease inhibitor
CC mixture. The troponin I is then separated from the extract by affinity
CC chromatography in the presence of the extraction buffer and calcium ions
CC thereby to absorb the troponin I. The troponin I is then described by
CC washing with the aqueous extraction buffer containing EGTA. The protease
CC inhibitor mixture used comprises at least two cathepsin protease
CC inhibitors, at least one serine protease inhibitor and at least one
CC cysteine protease inhibitor. The inhibitor mixture may also contain an
CC aspartate protease inhibitor, an aminopeptidase protease inhibitor and
CC a metalloendo-peptidase inhibitor. The isolated troponin I can be used as
CC a standard in detection assays for early detection of myocardial
CC infarction. The method provides pure and stable troponin which can
CC provide for reproducible and reliable clinical testing.
SQ Sequence 31 AA;

Query Match 29.6%; Score 202; DB 21; Length 31;
Best Local Similarity 100.0%; Pred. No. 4.88e-09;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 adgssdaareppapapirrrssnyrayate 31
|||||
Qy 2 ADGSSDAAREPPAPAPIRRRSSNYRAYATE 32

RESULT 14

ID R73052 standard; peptide; 31 AA.
AC R73052;
DT 14-DEC-1995 (first entry)
DE N-terminal sequence of cardiac troponin I.
KW Cardiac troponin I; cTnI; N-terminal region; cardiac specific;
KW protease inhibitor; myocardial infarction.
OS Homo sapiens.

PN CA2130280-A.
PD 25-FEB-1995.
PF 17-AUG-1994; 130280.
PR 24-AUG-1993; US-110824.
PA (SPEC-) SPECTRAL DIAGNOSTICS INC.
PI Jackowski G, Lee L;
DR WPI: 95-155575/21.
PT New intact cardiac troponin I from heart tissue - isolated in
PT presence of urea and protease inhibitors, useful as calibrator and
PT quality control standard for troponin assay.
PS Claim 8; Page 6; 30pp; English.
CC The sequence shown is the N-terminal sequence of cardiac troponin I
CC (cTnI). This sequence was used in the development of a method for
CC purifying cardiac troponin I with increased stability. The method was
CC to extract the cTnI in the presence of a mixture of protease inhibitors.
CC This mixture of protease inhibitors includes at least 2 cathepsin
CC protease inhibitors, at least 1 serine protease inhibitor and at least
CC 1 cysteine protease inhibitor. This mixture is effective to inhibit
CC degradation of the cardiac specific N-terminal region of cTnI, which is
CC this sequence. The advantage of this method is that it enables
CC practically intact cTnI that has good storage stability to be isolated.
CC The cTnI may then be used as a sensitive early indicator of myocardial
CC infarction.
SQ Sequence 31 AA;

Query Match 29.6%; Score 202; DB 14; Length 31;
Best Local Similarity 100.0%; Pred. No. 4.88e-09;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 adgssdaareppapapirrrssnyrayate 31
|||||
Qy 2 ADGSSDAAREPPAPAPIRRRSSNYRAYATE 32

RESULT 15

ID W22598 standard; protein; 182 AA.
AC W22598;
DT 23-MAR-1998 (first entry)
DE Human fast twitch skeletal muscle troponin I.
KW Human; fast twitch skeletal muscle troponin; angiogenesis; inhibitor;
KW tumour; ocular neovascularisation; arthritis; psoriasis;
KW atherosclerotic plaque; nonunion fracture.
OS Homo sapiens.
PN W09730085-A1.
PD 21-AUG-1997; U02439.
PF 14-FEB-1997; US-602941.
PR 16-FEB-1996; US-602941.
PA (CHIL-) CHILDRENS MEDICAL CENT.
PI Langer RS, Moses MA, Sytkowski A, Wiederschain DG,
PI Wu I;
DR WPI: 97-424977/39.
PT Use of troponin subunits as angiogenesis inhibitors - used for
PT treating e.g. tumours, ocular neovascularisation, arthritis,
PT psoriasis, atherosclerotic plaques or nonunion fractures
PS Claim 1; Page 9; 51pp; English.
CC A novel pharmaceutical composition has been developed which comprises a
CC carrier and an angiogenesis inhibiting amount of a peptide which is:
CC (a) an inhibitor of basic fibroblast growth factor (bFGF)-stimulated
CC bovine endothelial cell proliferation having an IC50 of at least
CC 10 nM; (b) greater than 75 amino acids in length; and (c) greater
CC than 80% homologous with a subunit selected from human fast-twitch
CC troponin subunit C, subunit I or subunit T. The present sequence
CC represents human fast-twitch troponin subunit I. The compositions can
CC be used for inhibiting atopic angiogenesis. They can be used to treat a
CC cancerous condition, or to prevent progression from a pre-neoplastic or
CC non-malignant state into a neoplastic or a malignant state. They can
CC also be used to treat ocular disorders associated with
CC neovascularisation such as neovascular glaucoma, diabetic retinopathy,
CC retinoblastoma, retrolental fibroplasia, uveitis, retinopathy of
CC prematurity, macular degeneration, corneal graft neovascularisation as
CC well as other eye inflammatory diseases, ocular tumour and diseases
CC associated with choroidal or iris neovascularisation. They can also be
CC used to treat other disorders e.g. haemangioma, arthritis, psoriasis,

CC angiofibroma, atherosclerotic plaques, delayed wound healing,
CC granulations, haemophilic joints, hypertrophic scars, nonunion
CC fractures, Osler-Weber syndrome, pyogenic granuloma, scleroderma,
CC trachoma, and vascular adhesions.
SQ Sequence 182 AA;
Query Match 29.5%; Score 201; DB 26; Length 182;
Best Local Similarity 39.7%; Pred. No. 5.99e-09;
Matches 25; Conservative 21; Mismatches 16; Indels 1; Gaps 1;
Db 6 knraitarrqhlksvmlqiaatelekesrreaekqnylaehcpplhipg-smsevqel 64
Qy 37 KKSKLSASRKQLQLTLLQIAKQELERAEERRGKGRALSTRCPLELAGLGFALQDL 96
Db 65 ckq 67
Qy 97 CRQ 99
Search completed: Fri Jan 21 14:31:17 2000
Job time : 60 secs.

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W E S R E H (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jan 21 14:29:29 2000; MasPar time 6.59 Seconds

Tabular output not generated. 602.084 Million cell updates/sec

Title: >US-09-176-546-2

Description: (1-99) from US09176546.pap

Perfect Score: 682

Sequence: 1 MADGSSDAAREPRAPAPR.....CQPLELAGLFAELQDLQCR 99

Scoring table: PAM 150

Gap 11

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: pir60

1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 40.178; Variance 87.144; scale 0.461W

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	682	100.0	210	1	TPHUIC	troponin I, cardiac m
2	614	90.0	211	2	A53805	troponin I, cardiac -
3	610	89.4	211	2	A60124	troponin I, cardiac m
4	608	89.1	211	2	I56441	troponin I - rat
5	592	86.8	216	1	TPRBIC	troponin I, cardiac m
6	585	85.9	211	2	A29994	troponin I, cardiac m
7	431	63.2	208	2	A41030	troponin I, cardiac m
8	429	62.9	244	2	I51408	cardiac troponin I -
9	237	34.8	187	2	B44786	troponin I, slow skel
10	231	33.9	187	1	TPHUW	troponin I, slow skel
11	219	32.1	184	1	TPRBIW	troponin I, slow skel
12	210	30.8	142	2	JC5611	troponin I alpha - se
13	209	30.6	142	2	JC5612	troponin I beta - sea
14	208	30.5	182	1	TPRBIS	troponin I, fast skel
15	205	30.1	182	2	A44786	troponin I, fast skel
16	201	29.5	182	1	TPHUIS	troponin I, fast skel
17	193	28.3	173	2	JC5610	troponin I - sea squi
18	192	28.2	183	2	A23569	troponin I, fast skel
19	192	28.2	183	1	TPCHIS	troponin I, fast skel
20	152	22.3	176	2	S70008	troponin I - Atlantic
21	144	21.1	208	2	A40547	troponin I - fruit fl
22	143	21.0	260	2	B38594	troponin I - fruit fl
23	136	19.9	201	2	A31484	troponin I, fast skel

24	123	18.0	208	2	A38594	troponin I - fruit fl	1.39e-04
25	105	15.4	292	2	JE0233	troponin-I - scallop	3.75e-02
26	101	14.8	258	2	I53021	troponin T - human	1.23e-01
27	101	14.8	886	2	S07132	hypothetical protein	1.23e-01
28	100	14.7	295	2	D56279	coxL 3'-region hypoth	1.64e-01
29	93	13.6	234	2	B44459	troponin T, fast skel	1.21e+00
30	93	13.6	249	2	A44459	troponin T, fast skel	1.21e+00
31	93	13.6	266	1	TPRBT5	troponin T, fast skel	1.21e+00
32	92	13.5	272	2	A24824	troponin T, fast skel	1.60e+00
33	90	13.2	140	2	I38855	centromere protein-A	2.77e+00
34	90	13.2	314	2	JC4951	troponin T - scallop	2.77e+00
35	90	13.2	399	2	G71242	probable 26S proteina	2.77e+00
36	90	13.2	410	2	C69197	ATP-dependent 26S pro	2.77e+00
37	90	13.2	518	2	C70887	probable Propionyl-Co	2.77e+00
38	90	13.2	564	2	S73615	threonine--tRNA ligas	2.77e+00
39	90	13.2	1992	2	A47297	myosin heavy chain fo	2.77e+00
40	89	13.0	382	1	A44056	nucleocapsid protein	3.64e+00
41	89	13.0	484	2	JU0091	sucrose alpha-glucosi	3.64e+00
42	88	12.9	289	2	D71475	probable AMP nucleosi	4.77e+00
43	88	12.9	810	2	S67050	probable membrane pro	4.77e+00
44	87	12.8	693	2	A29607	phenylalanine ammonia	6.24e+00
45	87	12.8	716	2	A56628	phenylalanine ammonia	6.24e+00

ALIGNMENTS

RESULT 1

ENTRY	TPHUIC	#type complete
TITLE	troponin I, cardiac muscle - human	
ORGANISM	#formal_name Homo sapiens	#common_name man
DATE	03-May-1994	#sequence_revision 03-May-1996
	05-Sep-1997	#text_change
ACCESSIONS	A61229; JN0837; S11522; A33185; S63690	
REFERENCE	A61229	
#authors	Hunkeler, N.M.; Kullman, J.; Murphy, A.M.	
#journal	Circ. Res. (1991) 69:1409-1414	
#title	Troponin I isoform expression in human heart.	
#cross-references	MUID:92035427	
#accession	A61229	
#status	not compared with conceptual translation	
#molecule_type	mRNA	
#residues	1-210	#label HUN
REFERENCE	JN0837	
#authors	Armour, K.L.; Harris, W.J.; Tempest, P.R.	
#journal	Gene (1993) 131:287-292	
#title	Cloning and expression in Escherichia coli of the cDNA encoding human cardiac troponin I.	
#cross-references	MUID:94010323	
#accession	JN0837	
#molecule_type	mRNA	
#residues	1-210	#label AR2
#cross-references	GB:M64247; NID:G339966; PID:G339967	
REFERENCE	S11522	
#authors	Vallins, W.J.; Brand, N.J.; Dabhadre, N.; Butler-Browne, G.;	
#journal	FEBS Lett. (1990) 270:57-61	
#title	Molecular cloning of human cardiac troponin I using polymerase chain reaction.	
#cross-references	MUID:91032031	
#accession	S11522	
#molecule_type	mRNA	
#residues	1-85, T' 87-210	#label VAL
#cross-references	EMBL:X54163; NID:937427; PID:937428	
REFERENCE	S12886	
#authors	Mittmann, K.; Jaquet, K.; Heilmeyer Jr., L.M.G.	
#journal	FEBS Lett. (1990) 273:41-45	
#title	A common motif of two adjacent phosphoserines in bovine, rabbit and human cardiac troponin I.	
#cross-references	MUID:91032199	
#contents	annotation; acetylated amino end; phosphorylation sites	
GENETICS		
#gene	GDB:TNNT3	
#cross-references	GDB:125309; OMIM:191044	

```

#map_position 19p13.2-19q13.2
COMPLEX
troponin is a heterotrimer with one molecule each of troponin
C (calcium binding component), troponin I (inhibitory
component), and troponin T (tropomyosin-binding component)
FUNCTION
#description binds actin and inhibits myosin ATPase activity; with
tropomyosin mediates contraction of vertebrate striated
muscle in response to calcium
#pathway muscle contraction
CLASSIFICATION #superfamily troponin I
KEYWORDS acetylated amino end; actin binding; cardiac muscle; heart;
muscle contraction; phosphoprotein
FEATURE
2 #modified_site acetylated amino end (Ala) (in mature
form) #status experimental
23,24 #binding_site phosphate (Ser) (covalent) (by
CAMP-dependent kinase) #status experimental
SUMMARY #length 210 #molecular-weight 24007 #checksum 1669
Query Match 100.0%; Score 682; DB 1; Length 210;
Best Local Similarity 100.0%; Pred. No. 1.31e-103;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 MADGSSDAAREPPAPAPIRRRSSNYRAYATEPHAKKSKISASRKLQTLMLQIAKQ 60
QY 1 MADGSSDAAREPPAPAPIRRRSSNYRAYATEPHAKKSKISASRKLQTLMLQIAKQ 60
Db 61 LERAEERREKGRALSTRCQPLELAGLGFAGLQDLQCRQ 99
QY 61 LERAEERREKGRALSTRCQPLELAGLGFAGLQDLQCRQ 99
RESULT 2
ENTRY #type complete
TITLE troponin I, cardiac - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change
KEYWORDS NH-2-terminal peptide in myofilament activation.
#cross-references MUID:94253083
#accession A53805
#status preliminary
#molecule_type mRNA
#residues 1-211 #label GUO
#cross-references GB:009181; NID:9484093; PID:g508866
REFERENCE A53108
#authors Ausoni, S.; Campione, M.; Picard, A.; Moretti, P.; Vitadello,
M.; De Nardi, C.; Schiaffino, S.
#journal J. Biol. Chem. (1994) 269:339-346
#title Structure and regulation of the mouse cardiac troponin I
#keywords Structure and regulation of the mouse cardiac troponin I
#cross-references MUID:94103233
#accession A53108
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-211 #label RES
#cross-references EMBL:Z22784; NID:g313104; PID:g313105
GENETICS
#introns 4/2; 8/3; 37/3; 51/3; 95/3; 125/3; 184/3
CLASSIFICATION #superfamily troponin I
KEYWORDS actin binding; heart; phosphoprotein
SUMMARY #length 211 #molecular-weight 24259 #checksum 7181
Query Match 90.0%; Score 614; DB 2; Length 211;
Best Local Similarity 89.0%; Pred. No. 8.63e-91;
Matches 89; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

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Db 1 MADSSDAAGEPPAPAPVRRSSNYRAYATEPHAKKSKISASRKLQTLMLQIAKQ 60
QY 1 MADGSSDAAREPPAPAPIRRRSS-NYRAYATEPHAKKSKISASRKLQTLMLQIAKQ 59
Db 61 EMERAEERREKGRVLTTRCQPLELDGLGFEEQLQDLQCRQ 100
QY 60 ELERAEERREKGRALSTRCQPLELAGLGFAGLQDLQCRQ 99
RESULT 3
ENTRY #type complete
TITLE troponin I, cardiac muscle - rat
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change
ACCESSIONS A60124
REFERENCE A60124; A38398; S14849
#authors Ausoni, S.; De Nardi, C.; Moretti, P.; Gorza, L.; Schiaffino,
S.
#journal Development (1991) 112:1041-1051
#title Developmental expression of rat cardiac troponin I mRNA.
#accession A60124
#molecule_type mRNA
#residues 1-211 #label AUS
#cross-references EMBL:X58499; NID:g56022; PID:g56023
REFERENCE A38398
#authors Murphy, A.M.; Jones II, L.; Sims, H.F.; Strauss, A.W.
#journal Biochemistry (1991) 30:707-712
#title Molecular cloning of rat cardiac troponin I and analysis of
troponin I isoform expression in developing rat heart.
#cross-references MUID:91105162
#accession A38398
#molecule_type mRNA
#residues 1-211 #label MUR
#cross-references GB:M57679; GB:J05304; NID:g207509; PID:g207510
CLASSIFICATION #superfamily troponin I
KEYWORDS actin binding; cardiac muscle; heart
SUMMARY #length 211 #molecular-weight 24159 #checksum 7678
Query Match 89.4%; Score 610; DB 2; Length 211;
Best Local Similarity 89.0%; Pred. No. 4.87e-90;
Matches 89; Conservative 4; Mismatches 6; Indels 1; Gaps 1;
Db 1 MADSSDAAGEPPAPAPVRRSSNYRAYATEPHAKKSKISASRKLQTLMLQIAKQ 60
QY 1 MADGSSDAAREPPAPAPIRRRSS-NYRAYATEPHAKKSKISASRKLQTLMLQIAKQ 59
Db 61 EMERAEERREKGRVLTTRCQPLELDGLGFEEQLQDLQCRQ 100
QY 60 ELERAEERREKGRALSTRCQPLELAGLGFAGLQDLQCRQ 99
RESULT 4
ENTRY #type complete
TITLE troponin I - rat
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
ACCESSIONS I56441
REFERENCE I56441
#authors Martin, A.F.; Orłowski, J.
#journal J. Mol. Cell. Cardiol. (1991) 23:583-588
#title Molecular cloning and developmental expression of the rat
cardiac-specific isoform of troponin I.
#cross-references MUID:91359315
#accession I56441
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-211 #label RES
#cross-references GB:M92074; NID:g207515; PID:g207516
CLASSIFICATION #superfamily troponin I
SUMMARY #length 211 #molecular-weight 24163 #checksum 7943

```

#authors

REFERENCE
A41030

REFERENCE
A41030

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#journal J. Biol. Chem. (1991) 266:19659-19665
#title Structure and developmental expression of troponin I
#isoforms. cDNA clone analysis of avian cardiac troponin I
#mRNA:
#cross-references MUID:92011768
#accession A41030
#molecule_type mRNA
#residues 1-208 #label HAS
#cross-references GB:M73702; NID:g213647; PID:g213648
CLASSIFICATION #superfamily troponin I
KEYWORDS actin binding; cardiac muscle; heart
SUMMARY #length 208 #molecular-weight 23601 #checksum 578

Query Match 63.2%; Score 431; DB 2; Length 208;
Best Local Similarity 67.4%; Pred. No. 7,90e-57;
Matches 62; Conservative 12; Mismatches 17; Indels 1; Gaps 1;

Db 2 AEEEPKPPPPRRKSSANYRAYVEPHAKRKSISASRKLQKTLTLLQAKRDLEERQEE 61
QY 9 AREPRPAPAPIRRRSS-NYRAYATEPHAKKKSISASRKLQKTLTLLQIAKQELERAAE 67
Db 62 RAGEKQRHGLGELCPPPELDGLGVAQLQELCRE 93
QY 68 RRGKGRALSTRCPQLEAGLGLFAELQDLQCRQ 99

RESULT 8
ENTRY I51408 #type complete
TITLE cardiac troponin I - African clawed frog
ORGANISM #formal_name Xenopus laevis #common_name African clawed frog
DATE 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Feb-1997
ACCESSIONS I51408
REFERENCE I51408
#authors Drysdale, T.A.; Tonissen, K.F.; Patterson, K.D.; Crawford, M.J.; Krieg, P.A.
#journal Dev. Biol. (1994) 165:432-441
#title Cardiac troponin I is a heart-specific marker in the Xenopus embryo: expression during abnormal heart morphogenesis.
#cross-references MUID:95046865
#accession I51408
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-244 #label DRY
#cross-references GB:L25721; NID:g410050; PID:g410051
CLASSIFICATION #superfamily troponin I
KEYWORDS heart
SUMMARY #length 244 #molecular-weight 28198 #checksum 1120

Query Match 62.9%; Score 429; DB 2; Length 244;
Best Local Similarity 60.0%; Pred. No. 1.83e-56;
Matches 60; Conservative 23; Mismatches 16; Indels 1; Gaps 1;

Db 25 VAPEPKPAPPAPPPPLIRRRSSANYRAYATEPQVRKPKISASRKLQNTMMLQIAKA 84
QY 1 MADGSDAAEPPAPAPIRRRSS-NYRAYATEPHAKKKSISASRKLQKTLTLLQIAKQ 59
Db 85 EMREEEERAREKRYLAECQPLQLSLGRSELODLCQE 124
QY 60 ELEREAERGERGRALSTRCPQLEAGLGLFAELQDLQCRQ 99

RESULT 9
ENTRY B44786 #type complete
TITLE troponin I, slow skeletal muscle - rat
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 19-Mar-1993 #sequence_revision 19-Mar-1993 #text_change 17-Mar-1999
ACCESSIONS B44786
REFERENCE A44786
#authors Koppe, R.I.; Hallauer, P.L.; Karpatti, G.; Hastings, K.E.M.
#journal J. Biol. Chem. (1989) 264:14327-14333
#title cDNA clone and expression analysis of rodent fast and slow
```

```
#cross-references MUID:89340548
#accession B44786
#status preliminary
#molecule_type mRNA
#residues 1-187 #label KOP
#cross-references GB:J04993; NID:g207517; PID:g207518
CLASSIFICATION #superfamily troponin I
KEYWORDS skeletal muscle
SUMMARY #length 187 #molecular-weight 21724 #checksum 7736

Query Match 34.8%; Score 237; DB 2; Length 187;
Best Local Similarity 53.7%; Pred. No. 1.68e-22;
Matches 36; Conservative 12; Mismatches 19; Indels 0; Gaps 0;

Db 2 PEVERKSKITASRKLMLKSLAKAKECWEHEERAEKRVYLSERIPTLOTGRLSLA 61
QY 33 PHAKKSKISASRKLQKTLTLLQIAKQELERAEERGERGRALSTRCPQLEAGLGLFAE 92
Db 62 LQDLCRE 68
QY 93 LQDLQCRQ 99

RESULT 10
ENTRY TPHUIW #type complete
TITLE troponin I, slow skeletal muscle - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 06-Jan-1995 #sequence_revision 03-May-1996 #text_change 18-Sep-1998
ACCESSIONS A53740; A53555
REFERENCE A53740
#authors Corin, S.J.; Juhasz, O.; Zhu, L.; Conley, P.; Kedes, L.; Wade, R.
#journal J. Biol. Chem. (1994) 269:10651-10659
#title Structure and expression of the human slow twitch skeletal muscle troponin I gene.
#cross-references MUID:94193765
#accession A53740
#molecule_type DNA
#residues 1-187 #label COR
#cross-references GB:L21905
REFERENCE A53555
#authors Wade, R.; Eddy, R.; Shows, T.B.; Kedes, L.
#journal Genomics (1990) 7:346-357
#title cDNA sequence, tissue-specific expression, and chromosomal mapping of the human slow-twitch skeletal muscle isoform of troponin I.
#cross-references MUID:90307007
#accession A53555
#molecule_type mRNA
#residues 1-181, NA, 184-187 #label WAD
#cross-references GB:J04760; NID:g339964; PID:g339965
GENETICS
#gene GDB:TNNI1
#map_position lq32-lq32
#introns 4/2; 5/3; 19/3; 63/3; 93/3; 152/3
#note the first intron occurs before the initiator codon
#complex troponin is a heterotrimer with one molecule each of troponin C (calcium binding component), troponin I (inhibitory component), and troponin T (tropomyosin-binding component)
FUNCTION
#description binds actin and inhibits myosin ATPase activity; with tropomyosin mediates contraction of vertebrate striated muscle in response to calcium
#pathway muscle contraction
CLASSIFICATION #superfamily troponin I
KEYWORDS acetylated amino end; actin binding; muscle contraction; skeletal muscle
FEATURE 2
#modified_site acetylated amino end (Pro) (in mature form) #status predicted
```



```

##cross-references GB:L04347
##experimental_source skeletal muscle
##note
sequence extracted from NCBI backbone (NCBIP:120236) and
corrected to correspond with the published sequence
the authors translated the codons GGC for residue 56 as
Gln, and TAT for residue 80 as Thr

REFERENCE
A93193
#authors
Wilkinson, J.M.; Grand, R.J.A.
#journal
Nature (1978) 271:31-35
#title
Comparison of amino acid sequence of troponin I from
different striated muscles.
#cross-references MUID:78114026
#accession
A93193
##molecule_type protein
##residues
2-154,158-182 #label WIL
REFERENCE
A90286
#authors
Wilkinson, J.M.; Grand, R.J.A.
#journal
Biochem. J. (1975) 149:493-496
#title
The amino acid sequence of troponin I from rabbit skeletal
muscle.
#cross-references MUID:76039510
#accession
A90286
##molecule_type protein
##residues
2-114,'R',115-154,158-182 #label W12
REFERENCE
A91408
#authors
Moir, A.J.G.; Wilkinson, J.M.; Perry, S.V.
#journal
FEBS Lett. (1974) 42:253-256
#title
The phosphorylation sites of troponin I from white skeletal
muscle of the rabbit.
#cross-references MUID:74309023
#contents
annotation; phosphorylation sites
REFERENCE
A91407
#authors
Huang, T.S.; Bylund, D.B.; Stull, J.T.; Krebs, E.G.
#journal
FEBS Lett. (1974) 42:249-252
#title
The amino acid sequences of the phosphorylated sites in
troponin-I from rabbit skeletal muscle.
#cross-references MUID:74308154
#contents
annotation; phosphorylation sites
REFERENCE
I46471
#authors
Putney, S.D.; Herlihy, W.C.; Schimmel, P.
#journal
Nature (1983) 302:718-721
#title
A new troponin T and cDNA clones for 13 different muscle
proteins, found by shotgun sequencing.
#cross-references MUID:83167564
#accession
I46514
##status
preliminary; translated from GB/EMBL/DBJ
##molecule_type mRNA
##residues
166-178 #label PUT
#cross-references EMBL:V00898; NID:g1738; PID:g929767
troponin is a heterotrimer with one molecule each of troponin
C (calcium binding component), troponin I (inhibitory
component), and troponin T (tropomyosin-binding component)

FUNCTION
#description
binds actin and inhibits myosin ATPase activity; with
tropomyosin mediates contraction of vertebrate striated
muscle in response to calcium
#pathway
muscle contraction
#superfamily troponin I
KEYWORDS
acetylated amino end; actin binding; muscle contraction;
phosphoprotein; skeletal muscle
FEATURE
2
#modified site acetylated amino end (Gly) (in mature
form) #status experimental
12
#binding site phosphate (Thr) (covalent) (by
cAMP-dependent kinase) #status experimental
20,90,118
#binding site phosphate (Ser) (covalent) (by
cAMP-dependent kinase) #status experimental
SUMMARY
#length 182 #molecular-weight 21214 #checksum 8861

Query Match 30.5%; Score 208; DB 1; Length 182;
Best Local Similarity 42.9%; Pred. NO. 1.12e-17;
Matches 27; Conservative 19; Mismatches 16; Indels 1; Gaps 1;

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```

Db 6 KNRRAITARRQHLKSVMLQIAATAELEKEBGRRAEKQNYLAECPPPLSLPG-SMAEVOEL 64
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 37 KKSISASRKQLKLTLLQIAKQELEREAEERGERGKRALSTRCPQLELAGLGFALQDL 96
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 65 CKQ 67
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 97 CRQ 99

RESULT 15
ENTRY A44786 #type complete
TITLE troponin I, fast skeletal muscle - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 19-Mar-1993 #sequence_revision 19-Mar-1993 #text_change
17-Mar-1999
ACCESSIONS A44786
REFERENCE A44786
#authors Koppe, R.I.; Hallauer, P.L.; Karpatis, G.; Hastings, K.E.M.
#journal J. Biol. Chem. (1989) 264:14327-14333
#title cDNA clone and expression analysis of rodent fast and slow
skeletal muscle troponin I mRNAs.
#cross-references MUID:89340548
#accession A44786
##status preliminary
##molecule_type mRNA
##residues 1-182 #label KOP
#cross-references GB:J04992; NID:g202164; PID:g202165
CLASSIFICATION #superfamily troponin I
KEYWORDS skeletal muscle
SUMMARY #length 182 #molecular-weight 21357 #checksum 306

Query Match 30.1%; Score 205; DB 2; Length 182;
Best Local Similarity 41.3%; Pred. No. 3.49e-17;
Matches 26; Conservative 20; Mismatches 16; Indels 1; Gaps 1;
Db 6 KNRRAITARRQHLKSVMLQIAATAELEKEBGRRAEKQNYLAECPPPLSLPG-SMAEVOEL 64
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 37 KKSISASRKQLKLTLLQIAKQELEREAEERGERGKRALSTRCPQLELAGLGFALQDL 96
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 65 CKQ 67
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 97 CRQ 99

Search completed: Fri Jan 21 14:29:58 2000
Job time : 29 secs.

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Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	252	37.0	188	13	O90350	TROPONIN I SLOW SKELET	4.47e-27
2	210	30.8	142	5	O01355	LARVAL TROPONIN I BETA	1.54e-19
3	209	30.6	142	5	O01356	LARVAL TROPONIN I ALPHA	2.31e-19
4	193	28.3	173	5	O01354	TROPONIN I.	1.43e-16
5	180	26.4	229	5	O77010	TROPONIN I.	2.43e-14
6	163	23.9	176	13	O90365	TROPONIN-I.	1.73e-11
7	161	23.6	172	13	O13095	TROPONIN-I ISOFORM 3.	3.71e-11
8	160	23.5	180	13	O13094	TROPONIN-I ISOFORM 2.	5.42e-11
9	152	22.3	176	13	O90366	TROPONIN-I.	1.10e-09
10	117	17.2	172	13	O13093	FAST MYOTOMAL MUSCLE T	2.99e-04
11	106	15.5	817	4	O75420	ORF2.	1.14e-02
12	105	15.4	271	5	O64077	TROPONIN I (FRAGMENT).	1.58e-02
13	104	15.2	293	5	O15988	TROPONIN I.	2.18e-02
14	104	15.2	314	5	O15987	TROPONIN I.	2.18e-02
15	104	15.2	314	5	O15987	SIMILAR TO TROPONIN I.	5.65e-02
16	101	14.8	306	5	O23585	ATP OPERON (FRAGMENT).	5.65e-02
17	100	14.7	885	2	O53031	COXMSL GENE CLUSTER.	7.73e-02
18	98	14.4	295	2	O51326	PSNF2L.	1.44e-01
19	98	14.4	1422	5	O00914	PSNF2L.	1.44e-01
20	97	14.2	197	5	O44572	W3F8.1 PROTEIN.	1.97e-01
21	97	14.2	574	4	O75134	K1AA0639 PROTEIN (FRAG	1.97e-01

```

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
CN TELEOSTEI; CLUPEOMORPHA; CLUPEIDAE; CLUPEINAE; CLUPEA.
[1]
RC SEQUENCE FROM N.A.
RP STRAIN=CLYDE-STOCK (BUCHAN BANK); TISSUE=WHOLE ORGANISM;
RA HODGSON P.A., LEAVER M.J., GEORGE S.G.;
RL SUBMITTED (JAN-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR EMBL; F020111; G643662; -.
DR PFAM; PF00992; Troponin; 1.
SQ SEQUENCE 176 AA; 19641 MW; E2E04DAB CRC32;
Query Match 23.9%; Score 163; Length 176;
Best Local Similarity 36.7%; Pred. No. 1,73e-11;
Matches 22; Conservative 19; Mismatches 18; Indels 1; Gaps 1
Db 5 KMTSRKHLKSLVMTAATLEQAPADAAIAAKETIYSDNCPSLDYP5-STEDLOKLCKE 63
QY 40 KISASRKLQKLTLLQIAQKLEAEAEERKEGKAUSTRCOPLAGLIGFAEQLDLCRQ 99

```


[illegible]

QY 8 AAREPPAPAPIRRRSSNYRAYATEPHAKK-KSKISAS-RKLQKTLT-LQI-AKOELER 63

Db 570 QPP-PR-EPARAQAPN-HRYOLGGLGTAPLNQ 598
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 QY 64 EAERREKGRALSTRCPLELAGLFAELQD 95

RESULT 12
 ID Q44077 PRELIMINARY; PRT; 271 AA.
 AC Q44077;
 DT 01-JUN-1998 (TREMREL. 06, CREATED)
 DT 01-JUN-1998 (TREMREL. 06, LAST SEQUENCE UPDATE)
 DT 01-JUN-1998 (TREMREL. 06, LAST ANNOTATION UPDATE)
 DE TROPONIN I (FRAGMENT).
 OS CHLAMY NIPPONENSIS AKAZARA (AKAZARA SCALLOP) (JAPANESE SCALLOP).
 OC EUKARYOTA; METAZOA; MOLLUSCA; BIVALVIA; PTERIOMORPHIA; OSTREOIDA;
 OC PECTINIDAE; CHLAMY.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA NISHITA K., OJIMA T., SOEJIMA T.;
 RL SUBMITTED (DEC-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL; AB009368; D1024680;
 FT NON_TER 1
 SQ SEQUENCE 271 AA; 32068 MW; C9E22FB9 CRC32;

Query Match 15.4%; Score 105; DB 5; Length 271;
 Best Local Similarity 28.8%; Pred. No. 1.58e-02;
 Matches 17; Conservative 14; Mismatches 28; Indels 0; Gaps 0;

Db 123 LSPEKKMLKLMQKAEDLNEAKAKAEKYNIDLVKPFSTGDKVAAALQALCKD 181
 :: | | | | : : : : | | | | : :
 QY 41 ISASRLQLKTLTLLQIAKQELEREAEERGERGKRALSTRCPLELAGLFAELQDLCRQ 99

RESULT 13
 ID O15988 PRELIMINARY; PRT; 293 AA.
 AC O15988;
 DT 01-JAN-1998 (TREMREL. 05, CREATED)
 DT 01-JAN-1998 (TREMREL. 05, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMREL. 08, LAST ANNOTATION UPDATE)
 DE TROPONIN I.
 OS PATINOPECTEN YESSOENSIS (EZO GIANT SCALLOP) (YESSO SCALLOP).
 OC EUKARYOTA; METAZOA; MOLLUSCA; BIVALVIA; PTERIOMORPHIA; OSTREOIDA;
 OC PECTINIDAE; PATINOPECTEN.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA HOTTA A.L.;
 RL SUBMITTED (OCT-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL; AB008006; D1023723;
 DR PFAM; PF00992; TROPONIN; 1.
 SQ SEQUENCE 293 AA; 34670 MW; 49299FDE CRC32;

Query Match 15.2%; Score 104; DB 5; Length 293;
 Best Local Similarity 28.8%; Pred. No. 2.18e-02;
 Matches 17; Conservative 14; Mismatches 28; Indels 0; Gaps 0;

Db 145 LSPEKKMLKLMQKAEDLNEAKAKAEKYNIDLVKPFSTGDKVAAALQALCKD 203
 :: | | | | : : : : | | | | : :
 QY 41 ISASRLQLKTLTLLQIAKQELEREAEERGERGKRALSTRCPLELAGLFAELQDLCRQ 99

RESULT 14
 ID O15987 PRELIMINARY; PRT; 314 AA.
 AC O15987;
 DT 01-JAN-1998 (TREMREL. 05, CREATED)
 DT 01-JAN-1998 (TREMREL. 05, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMREL. 08, LAST ANNOTATION UPDATE)
 DE TROPONIN I.
 OS PATINOPECTEN YESSOENSIS (EZO GIANT SCALLOP) (YESSO SCALLOP).
 OC EUKARYOTA; METAZOA; MOLLUSCA; BIVALVIA; PTERIOMORPHIA; OSTREOIDA;
 OC PECTINIDAE; PATINOPECTEN.
 RN [1]
 RP SEQUENCE FROM N.A.

RA HOTTA A.L.;
 RL SUBMITTED (OCT-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL; AB008005; D1023722;
 DR PFAM; PF00992; TROPONIN; 1.
 SQ SEQUENCE 314 AA; 37009 MW; EBSA2098 CRC32;

Query Match 15.2%; Score 104; DB 5; Length 314;
 Best Local Similarity 28.8%; Pred. No. 2.18e-02;
 Matches 17; Conservative 14; Mismatches 28; Indels 0; Gaps 0;

Db 162 LSPEKKMLKLMQKAEDLNEAKAKAEKYNIDLVKPFSTGDKVAAALQALCKD 220
 :: | | | | : : : : | | | | : :
 QY 41 ISASRLQLKTLTLLQIAKQELEREAEERGERGKRALSTRCPLELAGLFAELQDLCRQ 99


RESULT 15
 ID Q23585 PRELIMINARY; PRT; 306 AA.
 AC Q23585;
 DT 01-NOV-1996 (TREMREL. 01, CREATED)
 DT 01-NOV-1996 (TREMREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMREL. 08, LAST ANNOTATION UPDATE)
 DE SIMILAR TO TROPONIN I. NCBI GI: 1072235.
 GN ZK721.2.
 OS CAENORHABDITIS ELEGANS.
 OC EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
 OC RHABDITINA; RHABDITOIDEA; RHABDITIIDAE; PELODERINAE; CAENORHABDITIS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 94150718.
 RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., COULSON A.,
 RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., FAVELLO A.,
 RA CRATON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
 RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
 RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
 RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
 RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
 RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
 RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans.";
 RL NATURE 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MILLER N.;
 RL SUBMITTED (NOV-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA WATERSTON R.;
 RL SUBMITTED (NOV-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL; U40951; G1072235;
 DR PFAM; PF00992; TROPONIN; 1.
 SQ SEQUENCE 306 AA; 35183 MW; C284B70F CRC32;

Query Match 14.8%; Score 101; DB 5; Length 306;
 Best Local Similarity 23.8%; Pred. No. 5.65e-02;
 Matches 20; Conservative 25; Mismatches 37; Indels 2; Gaps 2;

Db 65 MSEEAGEDA-QKAAERAKAEVKKRLEAEAGNKKKAKKGLTPERKKRLKLLMVKAAE 123
 :: | | | | : : : : | | | | : :
 QY 1 MADGSDAAREPPAPAPIRRRSSNYRAYATEPHAK-KSKISASRLQLKTLTLLQIAKQ 59

Db 124 DLKROQLLKEQEROKALADRTISL 147
 :: | | | | : : : : | | | | : :
 QY 60 ELEREAEERGERGKRALSTRCPLO 83

Search completed: Fri Jan 21 14:29:12 2000
 Job time : 52 secs.



 (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run On: Fri Jan 21 14:27:43 2000; MasPar time 4.57 Seconds

Tabular output not generated. 612.656 Million cell updates/sec

Title: >US-09-176-546-2

Description: (1-99) from US09176546.pap

Perfect Score: 682

Sequence: 1 MADGSSDAAREPRPAPAPR.....CQPLELAGLGFALQDLQCR 99

Scoring table: PAM 150

Gap 11

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: swiss-prot37

1:swissprot

Statistics: Mean 41.275; Variance 77.899; scale 0.530

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	671	98.4	209	1	TRIC_HUMAN	TROPONIN I, CARDIAC MU 1.63e-116
2	603	88.4	210	1	TRIC_MOUSE	TROPONIN I, CARDIAC MU 7.86e-102
3	599	87.8	210	1	TRIC_RAT	TROPONIN I, CARDIAC MU 5.70e-101
4	586	85.9	211	1	TRIC_BOVIN	TROPONIN I, CARDIAC MU 3.54e-98
5	539	79.0	206	1	TRIC_RABIT	TROPONIN I, CARDIAC MU 4.07e-88
6	431	63.2	207	1	TRIC_COTJA	TROPONIN I, CARDIAC MU 2.78e-65
7	429	62.9	243	1	TRIC_XENLA	TROPONIN I, CARDIAC MU 7.28e-65
8	288	39.3	168	1	TRIC_CHICK	TROPONIN I, CARDIAC MU 4.71e-32
9	237	34.8	186	1	TRIS_RAT	TROPONIN I, SLOW SKELE 5.03e-26
10	231	33.9	186	1	TRIS_HUMAN	TROPONIN I, SLOW SKELE 7.12e-25
11	219	32.1	184	1	TRIS_RABIT	TROPONIN I, SLOW SKELE 1.36e-22
12	208	30.5	181	1	TRIF_RABIT	TROPONIN I, FAST SKELE 1.60e-20
13	205	30.1	181	1	TRIF_MOUSE	TROPONIN I, FAST SKELE 5.81e-20
14	203	29.8	181	1	TRIF_RAT	TROPONIN I, FAST SKELE 1.37e-19
15	201	29.5	181	1	TRIF_HUMAN	TROPONIN I, FAST SKELE 3.22e-19
16	192	28.2	182	1	TRIF_CHICK	TROPONIN I, FAST SKELE 1.48e-17
17	143	21.0	259	1	TRI_DROME	TROPONIN I, (TNI) (WING 9.47e-08
18	136	19.9	201	1	TRI_PONLE	TROPONIN I, FAST SKELE 1.20e-03
19	110	16.1	564	1	FMRI_XENLA	FRAGILE X MENTAL RETAR 1.28e-02
20	103	15.1	548	1	FMRI_XENLA	FRAGILE X MENTAL RETAR 2.49e-02
21	101	14.8	257	1	TRT3_HUMAN	TROPONIN T, FAST SKELE 3.24e-01
22	93	13.6	278	1	TRT3_RABIT	CHITIN SYNTHASE (EC 2. 3.24e-01
23	93	13.6	886	1	CHS_SAPMO	

24	92	13.5	258	1	TRT3_RAT	TROPONIN T, FAST SKELE 4.43e-01
25	90	13.2	140	1	CENA_HUMAN	CENTROMERE PROTEIN A (8.19e-01
26	90	13.2	410	1	PRSI_METH	PUTATIVE 26S PROTEASE 8.19e-01
27	90	13.2	564	1	SYT_MYCPN	THREONYL-TRNA SYNTHETA 8.19e-01
28	89	13.0	382	1	NCAP_CVCAE	NUCLEOCAPSID PROTEIN. 1.11e+00
29	89	13.0	484	1	SCRE_VIBAL	SUCROSE-6-PHOSPHATE HY 1.11e+00
30	87	12.8	135	1	ZNTR_HAEIN	ZN(II)-RESPONSIVE REGU 2.03e+00
31	87	12.8	716	1	PALY_RHOTO	PHENYLALANINE AMMONIA- 2.03e+00
32	86	12.6	245	1	Y01A_MYCTU	HYPOPHETICAL 26.9 KD P 2.73e+00
33	86	12.6	294	1	HK5A_CHICK	HOMEOBOX PROTEIN NKX-2 2.73e+00
34	86	12.6	328	1	SGS3_DROER	SALIVARY GLUE PROTEIN 2.73e+00
35	86	12.6	468	1	BMP3_RAT	BONE MORPHOGENETIC PRO 2.73e+00
36	85	12.5	189	1	RL14_TRYBB	PROBABLE 40S RIBOSOMAL 3.66e+00
37	85	12.5	350	1	RS40_ARATH	ARGININE/SERINE-RICH S 3.66e+00
38	85	12.5	452	1	Y0A9_MYCTU	HYPOPHETICAL 47.5 KD P 3.66e+00
39	85	12.5	587	1	UL84_HCMVT	55 KD EARLY NONSTRUCTU 3.66e+00
40	85	12.5	614	1	FMRI_MOUSE	FRAGILE X MENTAL RETAR 3.66e+00
41	85	12.5	632	1	FMRI_HUMAN	FRAGILE X MENTAL RETAR 3.66e+00
42	85	12.5	797	1	PAT1_YEAST	TOPOISOMERASE II-ASSOC 3.66e+00
43	84	12.3	282	1	YHPQ_YEAST	HYPOPHETICAL 32.1 KD P 4.91e+00
44	84	12.3	400	1	NIFV_ENTAG	HOMOCITRATE SYNTHASE (4.91e+00
45	84	12.3	614	1	RUI7_HUMAN	U1 SMALL NUCLEAR RIBON 4.91e+00

ALIGNMENTS

RESULT 1
 ID TRIC_HUMAN STANDARD; PRT; 209 AA.
 AC P19429;

DT 01-FEB-1991 (REL. 17, CREATED)

DT 01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)

DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)

DE TROPONIN I, CARDIAC MUSCLE.

GN TNN13 OR TNNC1.

OS HOMO SAPIENS (HUMAN).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;

OC PRIMATES; CATARRHINI; HOMINIDAE; HOMO.

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=HEART MUSCLE;

RX MEDLINE; 91032031.

RA VALLINS W.J., BRAND N.J., DABHADE N., BUTLER-BROWNE G.,

RA YACOB M.H., BARTON P.J.R.;

RT "Molecular cloning of human cardiac troponin I using polymerase chain

reaction.",

FEBS LETT. 270:57-61(1990).

RN [2]

RP REVISION TO 85, SEQUENCE FROM N.A.

RX MEDLINE; 94010323.

RA ARMOUR K.L., HARRIS W.J., TEMPEST P.R.;

RT "Cloning and expression in Escherichia coli of the cDNA encoding

human cardiac troponin I.,"

GENE 131:287-292(1993).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE; 92035427.

RA HUNKELER N.M., KULLMAN J., MURPHY A.M.;

RT "Troponin I isoform expression in human heart.,"

CIRC. RES. 69:1409-1414(1991).

RN [4]

RP SEQUENCE FROM N.A.

RX MEDLINE; 96299735.

RA BHAYASAR P.K., BRAND N.J., YACOB M.H., BARTON P.J.R.;

RT "Isolation and characterization of the human cardiac troponin I gene

(TNN13).,"

GENOMICS 35:11-23(1996).

CC "- FUNCTION: TROPONIN I IS THE INHIBITORY SUBUNIT OF TROPONIN, THE

THIN FILAMENT REGULATORY COMPLEX WHICH CONFERS CALCIUM-SENSITIVITY

TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.

CC "- TROPONIN I BINDS TO ACTIN-TROPOMYOSIN.

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EMBL; X54163; G37428; ALT_SEQ.
DR EMBL; M64247; G339967; -.
DR EMBL; X90780; E196058; -.
DR EMBL; X90781; E196058; JOINED.
DR EMBL; X90782; E196058; JOINED.
DR PIR; A61229; A61229.
DR MIM; I91044; -.
DR PFAM; PF00992; Troponin; 1.
KW MUSCLE PROTEIN; ACTIN-BINDING; ACETYLATION.

FT INIT_MET 0 0
FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
FT SITE 79 79 INVOLVED IN TNI-TNT INTERACTIONS.
FT SITE 96 96 INVOLVED IN TNI-TNT INTERACTIONS.
FT SITE 31 78 INVOLVED IN BINDING TNC.
FT DOMAIN 128 148 INVOLVED IN BINDING TNC AND ACTIN.
FT SEQUENCE 209 AA; 23876 MW; 2B551B3 CRC32;
SQ

Query Match 98.4%; Score 671; DB 1; Length 209;
Best Local Similarity 100.0%; Pred. No. 1.63e-116;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 AGSSDAAREPRPAPAPIRRRSSNYRAYATEPHAKKSKISASRKLQKLTLLQIAKQEL 60
QY 2 AGSSDAAREPRPAPAPIRRRSSNYRAYATEPHAKKSKISASRKLQKLTLLQIAKQEL 61
Db 61 ERAEEREGKGRALSTRCQPLAGLGFAGLQDLQCRQ 98
QY 62 ERAEEREGKGRALSTRCQPLAGLGFAGLQDLQCRQ 99

RESULT 2
ID TRIC_MOUSE STANDARD; PRT; 210 AA.
AC P48787;
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE TROPONIN I, CARDIAC MUSCLE.
GN TNN13.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94103233.
RA AUSONI S., CAMPIONE M., PICARD A., MORETTI P., VITTADELLO M.,
RA DE NARDI C., SCHIAFFINO S.;
RT "Structure and regulation of the mouse cardiac troponin I gene."
RL J. BIOL. CHEM. 269:339-346(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CD-1; TISSUE=HEART;
RX MEDLINE; 94253083.
RA GUO X., WATTANAPERMOOL J., PALMITER K.A., MURPHY A.M., SOLARO R.J.;
RA "Mutagenesis of cardiac troponin I. Role of the unique NH2-terminal
peptide in myofibril activation."
RT J. BIOL. CHEM. 269:15210-15216(1994).
RL J. BIOL. CHEM. 269:15210-15216(1994).
CC -!- FUNCTION: TROPONIN I IS THE INHIBITORY SUBUNIT OF TROPONIN. THE
CC THIN FILAMENT REGULATORY COMPLEX WHICH CONFERS CALCIUM-SENSITIVITY
CC TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.
CC -!- TROPONIN I BINDS TO ACTIN-TROPOMYOSIN.
CC
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CC EMBL; Z22784; G313105; -.
DR EMBL; U09181; G508866; -.
DR MGI; MGI-98783; TNN13.
DR PFAM; PF00992; Troponin; 1.
KW MUSCLE PROTEIN; ACTIN-BINDING; ACETYLATION.
FT INIT_MET 0 0
FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
FT SITE 80 80 INVOLVED IN TNI-TNT INTERACTIONS.
FT SITE 97 97 INVOLVED IN TNI-TNT INTERACTIONS.
FT SITE 32 79 INVOLVED IN BINDING TNC.
FT DOMAIN 129 150 INVOLVED IN BINDING TNC AND ACTIN.
FT SEQUENCE 210 AA; 24127 MW; 14C53199 CRC32;
SQ

Query Match 88.4%; Score 603; DB 1; Length 210;
Best Local Similarity 88.9%; Pred. No. 7.86e-102;
Matches 88; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

Db 1 ADESSDAAGEPOPAPAPYRRSSNYRAYATEPHAKKSKISASRKLQKLTLLQIAKQ 60
QY 2 AGSSDAAREPRPAPAPIRRRSSNYRAYATEPHAKKSKISASRKLQKLTLLQIAKQ 60
Db 61 MEREAEEREGKGRVLRTRCQPLDGLGFEELQDLQCRQ 99
QY 61 LEREAEEREGKGRALSTRCQPLAGLGFAGLQDLQCRQ 99

RESULT 3
ID TRIC_RAT STANDARD; PRT; 210 AA.
AC P23693;
DT 01-NOV-1991 (REL. 20, CREATED)
DT 01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE TROPONIN I, CARDIAC MUSCLE.
GN TNN13 OR TNI OR CTNI.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91105162.
RA MURPHY A.M., JONES L. II, SIMS H.F., STRAUSS A.W.;
RA "Molecular cloning of rat cardiac troponin I and analysis of troponin
I isoform expression in developing rat heart."
RL BIOCHEMISTRY 30:707-712(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92037196.
RA AUSONI S., DE NARDI C., MORETTI P., GORZA L., SCHIAFFINO S.;
RA "Developmental expression of rat cardiac troponin I mRNA."
RL DEVELOPMENT 112:1041-1051(1991).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91359315.
RA MARTIN A.F., ORLOWSKI J.;
RA "Molecular cloning and developmental expression of the rat cardiac-
specific isoform of troponin I."
RL J. MOL. CELL. CARDIOL. 23:583-588(1991).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97218094.
RA MURPHY A.M., THOMPSON W.R., PENG L.F., JONES L.;
RA "Regulation of the rat cardiac troponin I gene by the transcription
factor GATA-4."
RL BIOCHEM. J. 322:393-401(1997).
CC -!- FUNCTION: TROPONIN I IS THE INHIBITORY SUBUNIT OF TROPONIN. THE
CC THIN FILAMENT REGULATORY COMPLEX WHICH CONFERS CALCIUM-SENSITIVITY
CC TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.
CC -!- TROPONIN I BINDS TO ACTIN-TROPOMYOSIN.
CC
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DR EMBL; M57679; G207510; -
DR EMBL; X58499; G56023; -
DR EMBL; M92074; G207516; -
DR EMBL; U77354; G1698958; -
DR PIR; A38398; A38398
DR PIR; A60124; A60124
DR PFAM; PF00992; Troponin; 1.
KW MUSCLE PROTEIN; ACTIN-BINDING; ACETYLATION.
FT INIT_MET 0
FT MOD_RES 1 ACETYLATION (BY SIMILARITY).
FT SITE 80 INVOLVED IN TNI-TNT INTERACTIONS.
FT SITE 97 INVOLVED IN TNI-TNT INTERACTIONS.
FT DOMAIN 32 INVOLVED IN BINDING TNC.
FT DOMAIN 129 INVOLVED IN BINDING TNC AND ACTIN.
FT CONFLICT 7 A -> S (IN REF. 3).
FT CONFLICT 181 I -> T (IN REF. 3).
SQ SEQUENCE 210 AA; 24028 MW; FEEB8E0 CRC32;

Query Match 87.8%; Score 599; DB 1; Length 210;
Best Local Similarity 88.9%; Pred. No. 5.70e-101;
Matches 88; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

Db 1 ADESSDAAGEQPAPAPVRRSSANRYAYATEPHAKKSKISASRKLQKLTMLQIAKOE 60
Qy 2 ADGSSDAAREPPAPAPIRRRSS-NRYAYATEPHAKKSKISASRKLQKLTMLQIAKOE 60
Db 61 MERAEREREGKGRVLTSCOPVLVDGLGFEQLDLCRQ 99
Qy 61 LEREAEREGKGRALSTRCPGLELAGLFAELQDLCRQ 99

RESULT 4
ID TRIC_BOVIN STANDARD; PRT; 211 AA.
AC P08057;
DT 01-AUG-1988 (REL. 08, CREATED)
DT 01-AUG-1988 (REL. 08, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE TROPONIN I, CARDIAC MUSCLE.
GN TNN13.
OS BOS TAURUS (BOVINE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC ARTIODACTYLA; RUMINANTIA; PECORA; BOVIDAE; BOVINAE; BOS.
RN [1]
RP SEQUENCE.
RX MEDLINE; 88294022.
RA LESZYK J., DUMASKALA R., POTTER J.D., COLLINS J.H.;
RT "Amino acid sequence of bovine cardiac troponin I.";
RL BIOCHEMISTRY 27:2821-2827(1988).
RN [2]
RP SEQUENCE.
RX MEDLINE; 88240346.
RA CREUTZ C.E., SNYDER S.L., HUSTED L.D., BEGGERLY L.K., FOX J.W.;
RT "Pattern of repeating aromatic residues in synexin. Similarity to the cytoplasmic domain of synaptophysin.";
RL BIOCHEM. BIOPHYS. RES. COMMUN. 152:1298-1303(1988).
CC -1- FUNCTION: TROPONIN I IS THE INHIBITORY SUBUNIT OF TROPONIN, THE THIN FILAMENT REGULATORY COMPLEX WHICH CONFERS CALCIUM-SENSITIVITY TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.
CC -1- TROPONIN I BINDS TO ACTIN-TROPOMYOSIN.
DR PIR; A29994; A29994.
DR PFAM; PF00992; Troponin; 1.
KW MUSCLE PROTEIN; ACTIN-BINDING; ACETYLATION; PHOSPHORYLATION.
FT MOD_RES 1 ACETYLATION.
FT SITE 81 INVOLVED IN TNI-TNT INTERACTIONS.
FT SITE 98 INVOLVED IN TNI-TNT INTERACTIONS.
FT DOMAIN 33 INVOLVED IN BINDING TNC.
FT DOMAIN 130 INVOLVED IN BINDING TNC AND ACTIN.

FT CONFLICT 16 16 P -> M (IN REF. 2).
SQ SEQUENCE 211 AA; 23922 MW; DAIDBEC0 CRC32;
Query Match 85.9%; Score 586; DB 1; Length 211;
Best Local Similarity 88.7%; Pred. No. 3.54e-98;
Matches 86; Conservative 6; Mismatches 3; Indels 2; Gaps 2;
Db 5 GGSTAG-DTVPAPPVRRSSANRYAYATEPHAKKSKISASRKLQKLTMLQIAKOE 63
Qy 4 GSSDAAREPPAPAPIRRRSS-NRYAYATEPHAKKSKISASRKLQKLTMLQIAKOE 62
Db 64 REAEEREGKGRALSTRCPGLELAGLFAELQDLCRQ 100
Qy 63 REAEEREGKGRALSTRCPGLELAGLFAELQDLCRQ 99

RESULT 5
ID TRIC_RABIT STANDARD; PRT; 206 AA.
AC P02646;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE TROPONIN I, CARDIAC MUSCLE.
GN TNN13.
OS ORYCTOLAGUS CUNICULUS (RABBIT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC LAGOMORPHA; LEPORIDAE; ORYCTOLAGUS.
RN [1]
RP SEQUENCE.
RX MEDLINE; 77087072.
RA GRAND R.J.A., WILKINSON J.M., MOLE L.E.;
RT "The amino acid sequence of rabbit cardiac troponin I.";
RL BIOCHEM. J. 159:633-641(1976).
RN [2]
RP REVISTON.
RX MEDLINE; 78060292.
RA GRAND R.J.A., WILKINSON J.M.;
RT "The amino acid sequence of rabbit slow-muscle troponin I.";
RL BIOCHEM. J. 167:183-192(1977).
RN [3]
RP PHOSPHORYLATION SITES.
RX MEDLINE; 76267707.
RA SOLARO R.J., MOIR A.J.G., PERRY S.V.;
RT "Phosphorylation of troponin I and the inotropic effect of adrenaline in the perfused rabbit heart.";
RL NATURE 262:615-617(1976).
CC -1- FUNCTION: TROPONIN I IS THE INHIBITORY SUBUNIT OF TROPONIN, THE THIN FILAMENT REGULATORY COMPLEX WHICH CONFERS CALCIUM-SENSITIVITY TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.
CC -1- PTM: SER-20 IS ONE OF THREE SITES IN THE REGION OF RESIDUES 1-48 THAT ARE PHOSPHORYLATED BY PHOSPHORYLASE KINASE.
CC -1- TROPONIN I BINDS TO ACTIN-TROPOMYOSIN.
DR PIR; A03090; TPRBIC.
DR PFAM; PF00992; Troponin; 1.
KW MUSCLE PROTEIN; ACTIN-BINDING; ACETYLATION; PHOSPHORYLATION.
FT MOD_RES 1 ACETYLATION (BY PHK).
FT MOD_RES 20 20 PHOSPHORYLATION (BY PHK).
FT SITE 75 75 INVOLVED IN TNI-TNT INTERACTIONS.
FT SITE 92 92 INVOLVED IN TNI-TNT INTERACTIONS.
FT DOMAIN 27 74 INVOLVED IN BINDING TNC.
FT DOMAIN 124 145 INVOLVED IN BINDING TNC AND ACTIN.
SQ SEQUENCE 206 AA; 23549 MW; D5690D26 CRC32;

Query Match 79.0%; Score 539; DB 1; Length 206;
Best Local Similarity 86.7%; Pred. No. 4.07e-88;
Matches 85; Conservative 4; Mismatches 5; Indels 4; Gaps 3;

Db 1 ADESSDAAGEARPAPA-VRR--SD-RAYATEPHAKKSKISASRKLQKLTMLQIAKOE 56
Qy 2 ADGSSDAAREPPAPAPIRRRSS-NRYAYATEPHAKKSKISASRKLQKLTMLQIAKOE 61
Db 57 EREAEREREGKGRALSTRCPGLELAGLFAELQDLCRQ 94

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QY 62 EREAEREGKGRALSTRCQPLEAGLGLFAELQDLQCRQ 99
      6
RESULT TRIC_CORJA STANDARD; PRT; 207 AA.
AC P27572;
DT 01-AUG-1992 (REL. 23, CREATED)
DT 01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE TROPONIN I, CARDIAC MUSCLE.
OS COTURNIX COTURNIX JAPONICA (JAPANESE QUAIL).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
OC NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; COTURNIX.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 92011768.
RA HASTINGS K.E., KOPPE R.I., MARMUR E., BADER D., SHIMADA Y.,
RA TOYOTA N.;
RT "Structure and developmental expression of troponin I isoforms. cDNA
RT clone analysis of avian cardiac troponin I mRNA.";
RL J. BIOL. CHEM. 266:19659-19665(1991).
CC -!- FUNCTION: TROPONIN I IS THE INHIBITORY SUBUNIT OF TROPONIN. THE
CC THIN FILAMENT REGULATORY COMPLEX WHICH CONFERS CALCIUM-SENSITIVITY
CC TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.
CC -!- TROPONIN I BINDS TO ACTIN-TROPOMYOSIN.
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CC
CC EMBL: L25721; G410051;
DR PFAM: PF00992; Troponin; 1.
DR MUSCLE PROTEIN; ACTIN-BINDING.
KW INIT_MET 0 0 BY SIMILARITY.
FT DOMAIN 9 14 POLY-GLU.
FT DOMAIN 17 22 POLY-GLU.
FT DOMAIN 84 91 POLY-GLU.
SQ SEQUENCE 207 AA; 23470 MW; 4B245E86 CRC32;

Query Match 63.2%; Score 431; DB 1; Length 207;
Best Local Similarity 67.4%; Pred. No. 2.78e-65;
Matches 62; Conservative 12; Mismatches 17; Indels 1; Gaps 1;

Db 1 AEEEPKPPPLRRSSNRYGYVPEPHAKROKISASRKLQKTLQLLQAKRLEREEQ 60
QY 9 AREPPAPAPIRRRSS-NRYAYATEPHAKKKSISASRKLQKTLQLLQAKLEERAAE 67

Db 61 RAGEKQRLGELCPPELDGLGVAQLQELCRE 92
QY 68 RRGKGRALSTRCQPLEAGLGLFAELQDLQCRQ 99

      7
RESULT TRIC_XENLA STANDARD; PRT; 243 AA.
AC P50754;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE TROPONIN I, CARDIAC MUSCLE (TROPONIN IC).
OS XENOPUS LAEVIS (AFRICAN CLAWED FROG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;
OC MESOBATRACHIA; PIPOIDEA; PIPIDAE; XENOPODINAE; XENOPUS.
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE-HEART MUSCLE;
RX MEDLINE: 95046865.
RA DRYSDALE T.A., TONISSEN K.F., PATTERSON K.D., CRAWFORD M.J.,
RA KRIEG P.A.;
RT "Cardiac troponin I is a heart-specific marker in the Xenopus embryo;

expression during abnormal heart morphogenesis.";
DEV. BIOL. 165:432-441(1994).
-!- FUNCTION: TROPONIN I IS THE INHIBITORY SUBUNIT OF TROPONIN. THE
THIN FILAMENT REGULATORY COMPLEX WHICH CONFERS CALCIUM-SENSITIVITY
TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.
-!- TISSUE SPECIFICITY: HEART.
-!- DEVELOPMENTAL STAGE: EXPRESSED AT ALL STAGES OF DEVELOPMENT.
-!- TROPONIN I BINDS TO ACTIN-TROPOMYOSIN.
CC
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CC
CC EMBL: L25721; G410051;
DR PFAM: PF00992; Troponin; 1.
DR MUSCLE PROTEIN; ACTIN-BINDING.
KW INIT_MET 0 0 BY SIMILARITY.
FT DOMAIN 9 14 POLY-GLU.
FT DOMAIN 17 22 POLY-GLU.
FT DOMAIN 84 91 POLY-GLU.
SQ SEQUENCE 243 AA; 28067 MW; 12B17823 CRC32;

Query Match 62.9%; Score 429; DB 1; Length 243;
Best Local Similarity 60.0%; Pred. No. 7.28e-65;
Matches 60; Conservative 23; Mismatches 16; Indels 1; Gaps 1;

Db 24 VAPEPKPPAPPAAPPLRRSSNRYAYATEPOVKRPKISASRKLQKTLQMLQIAKA 83
QY 1 MADGSSDAAREPPAPAPIRRRSS-NRYAYATEPHAKKKSISASRKLQKTLQIAQ 99

Db 84 EMREERERAREKERYLAECQPLQSLGSLRSELQDLQCE 123
QY 60 ELEREAEREGKGRALSTRCQPLEAGLGLFAELQDLQCRQ 99

      8
RESULT TRIC_CHICK STANDARD; PRT; 168 AA.
AC P27673;
DT 01-AUG-1992 (REL. 23, CREATED)
DT 01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
DT 01-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE)
DE TROPONIN I, CARDIAC MUSCLE (FRAGMENT).
OS GALLUS GALLUS (CHICKEN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
OC NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 92011768.
RA HASTINGS K.E., KOPPE R.I., MARMUR E., BADER D., SHIMADA Y.,
RA TOYOTA N.;
RT "Structure and developmental expression of troponin I isoforms. cDNA
RT clone analysis of avian cardiac troponin I mRNA.";
RL J. BIOL. CHEM. 266:19659-19665(1991).
CC -!- FUNCTION: TROPONIN I IS THE INHIBITORY SUBUNIT OF TROPONIN. THE
CC THIN FILAMENT REGULATORY COMPLEX WHICH CONFERS CALCIUM-SENSITIVITY
CC TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.
CC -!- TROPONIN I BINDS TO ACTIN-TROPOMYOSIN.
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CC
CC EMBL: M73703; G212821;
DR PFAM: PF00992; Troponin; 1.
DR MUSCLE PROTEIN; ACTIN-BINDING.

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OS      HOMO SAPIENS (HUMAN).
OC      EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC      PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
[1]
RN      SEQUENCE FROM N.A.
RP      MEDLINE; 90307007.
RX
RA      WADE R., EDDY R., SHOWS T.B., KEDES L.;
RT      "CDNA sequence, tissue-specific expression, and chromosomal mapping
RL      of the human slow-twitch skeletal muscle isoform of troponin I";
RL      GENOMICS 7:346-357(1990).
RN      [2]
RN      SEQUENCE FROM N.A.
RC      TISSUE-BLOOD;
RX      MEDLINE; 94193765.
RA      CORIN S.J., JUHASZ O., ZHU L., CONLEY P., KEDES L., WADE R.;
RT      "Structure and expression of the human slow twitch skeletal muscle
RL      troponin I gene.";
RL      J. BIOL. CHEM. 269:10651-10659(1994).
CC      -!- THIN FILAMENT REGULATORY COMPLEX WHICH CONFERS CALCIUM-SENSITIVITY
CC      TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.
CC      -!- TROPONIN I BINDS TO ACTIN-TROPOMYOSIN.
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CC      EMBL; J04760; G33965; -.
DR      EMBL; L21910; G437009; -.
DR      EMBL; L21906; G437009; JOINED.
DR      EMBL; L21908; G437009; JOINED.
DR      EMBL; L21909; G437009; JOINED.
DR      PIR; A35355; A35355.
DR      MIM; 191042; -.
DR      PFAM; PF00992; Troponin: 1.
KW      MUSCLE PROTEIN; ACTIN-BINDING.
FT      INIT-MET          0
FT      DOMAIN           1 47    INVOLVED IN BINDING TNC.
FT      DOMAIN           96 117   INVOLVED IN BINDING TNC AND ACTIN.
FT      CONFLICT         181 182   KS -> NA (IN REF. 1).
SQ      SEQUENCE        186 AA; 21561 MW; 6DABD050 CRC32;
Query Match              33.9%; Score 231; DB 1; Length 186;
Best Local Similarity 50.7%; Pred. No. 7.12e-25;
Matches 34; Conservative 14; Mismatches 19; Indels 0; Gaps 0;
Db
1 PEVERPKITASKLLKLSMLAKACEWEOHEEREAEKVYLAEPIQTGRGLSLA 60
| :||:||||| ||:|| | :||: ||| | :| | :||: ||:
QY 33 PHAKSKSIASRKLQTKLTLLQIAKELEAREEERGERGKRALSTRCPLEGAGFAE 92
| :||: ||| | :||: ||| | :||: ||| | :| | :||: ||:
Db 61 LDLCRE 67
| |||||
QY 93 LDLCRQ 99
| |||||
RESULT 11
ID TRIS_RABIT STANDARD; PRT; 184 AA.
AC P02645;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE TROPONIN I, SLOW SKELETAL MUSCLE (TROPONIN I, SLOW-TWITCH ISOFORM).
GN TNN1.
OS ORYCTOLAGUS CUNICULUS (RABBIT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC LAGOMORPHA; LEPORIDAE; ORYCTOLAGUS.
[1]
RN      MEDLINE. 78060292

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QY 97 CRQ 99
 RESULT 13
 ID TRIF_MOUSE STANDARD; PRT; 181 AA.
 AC P13412;
 DT 01-JAN-1990 (REL. 13, CREATED)
 DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DT TROPONIN I, FAST SKELETAL MUSCLE (TROPONIN I, FAST-TWITCH ISOFORM).
 GN TN12.
 DE MUS MUSCULUS (MOUSE).
 OS EUKARYOTA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89340548.
 RA KOPPE R.I., HALLAUER P.L., KARPATI G., HASTINGS K.E.M.;
 RT "CDNA clone and expression analysis of rodent fast and slow skeletal
 muscle troponin I mRNAs."
 RL J. BIOL. CHEM. 264:14327-14333(1989).
 CC -!- FUNCTION: TROPONIN I IS THE INHIBITORY SUBUNIT OF TROPONIN. THE
 CC THIN FILAMENT REGULATORY COMPLEX WHICH CONFERS CALCIUM-SENSITIVITY
 CC TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.
 CC -!- TROPONIN I BINDS TO ACTIN-TROPOMYOSIN.
 CC
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 CC
 CC EMBL; M73701; G206985; -.
 CC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89340548.
 RA KOPPE R.I., HALLAUER P.L., KARPATI G., HASTINGS K.E.M.;
 RT "CDNA clone and expression analysis of rodent fast and slow skeletal
 muscle troponin I mRNAs."
 RL J. BIOL. CHEM. 264:14327-14333(1989).
 CC -!- FUNCTION: TROPONIN I IS THE INHIBITORY SUBUNIT OF TROPONIN. THE
 CC THIN FILAMENT REGULATORY COMPLEX WHICH CONFERS CALCIUM-SENSITIVITY
 CC TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.
 CC -!- TROPONIN I BINDS TO ACTIN-TROPOMYOSIN.
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 CC
 CC EMBL; J04992; G202165; -.
 CC PIR; A44786; A44786.
 DR MGD; MGI:105070; TN12.
 DR PFAM; PF00992; TROPONIN; 1.
 DR HSP; P02643; 1A2X.
 KW MUSCLE PROTEIN; ACTIN-BINDING.
 FT INIT_MET 0 0
 FT DOMAIN 1 47 INVOLVED IN BINDING TNC.
 FT DOMAIN 96 116 INVOLVED IN BINDING TNC AND ACTIN.
 SQ SEQUENCE 181 AA; 21226 MW; BB5D5B61 CRC32;
 Query Match 30.1%; Score 205; DB 1; Length 181;
 Best Local Similarity 41.3%; Pred. No. 5.81e-20;
 Matches 26; Conservative 20; Mismatches 16; Indels 1; Gaps 1;
 Db 5 KNRRAITARRHKLQVLMQIAATELEKEESRESEKYNLSEHCPLHPG-SMSEVOEL 63
 QY 37 KSKISASRKLQKLLVLLQIAQELERAEERKEGKRALSTRCQPLELAGLGFALQDL 96
 Db 64 CKQ 66
 QY 97 CRQ 99
 RESULT 14
 ID TRIF_RAT STANDARD; PRT; 181 AA.
 AC P27768;
 DT 01-AUG-1992 (REL. 23, CREATED)
 DT 01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DT TROPONIN I, FAST SKELETAL MUSCLE (TROPONIN I, FAST-TWITCH ISOFORM).
 GN TN12 OR TRP1.
 DE OS RATTUS NORVEGICUS (RAT).
 OS EUKARYOTA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX GRAVEL M., HASTINGS K.E.;
 RA

FT INIT_MET 0 0 BY SIMILARITY.
FT DOMAIN 1 47 INVOLVED IN BINDING TNC.
FT DOMAIN 96 116 INVOLVED IN BINDING TNC AND ACTIN.
SQ SEQUENCE 181 AA; 21207 MW; 83ED65E4 CRC32;
Query Match 29.5%; Score 201; DB 1; Length 181;
Best Local Similarity 39.7%; Pred. No. 3.22e-19;
Matches 25; Conservative 21; Mismatches 16; Indels 1; Gaps 1;
Db 5 KNRATARRQHLSVMLQIAATELEKEESRRFAEKONYLAETHCPPLHIPG-SMSEVOEL 63
QY 37 KRSKISASRKLQKTLLELQIAKQELERAEERGERGKRALSTRCPLELAGLGFRELQDL 96
Db 64 CKQ 66
QY 97 CRQ 99

Search completed: Fri Jan 21 14:28:03 2000
Job time : 20 secs.